



computational course
Computational systems biology for
complex human disease:
from static to dynamic
representations of disease mechanisms

4–9 December 2022
Wellcome Genome Campus, UK



Building Molecular Maps using CellDesigner

WTAC

Computational Systems Biology for Complex Human Disease

Dr Anna Niarakis

Hinxton campus, December 5th 2022



Network construction

What is CellDesigner?

CellDesigner is a structured diagram editor for drawing gene-regulatory and biochemical networks that uses standard formats.

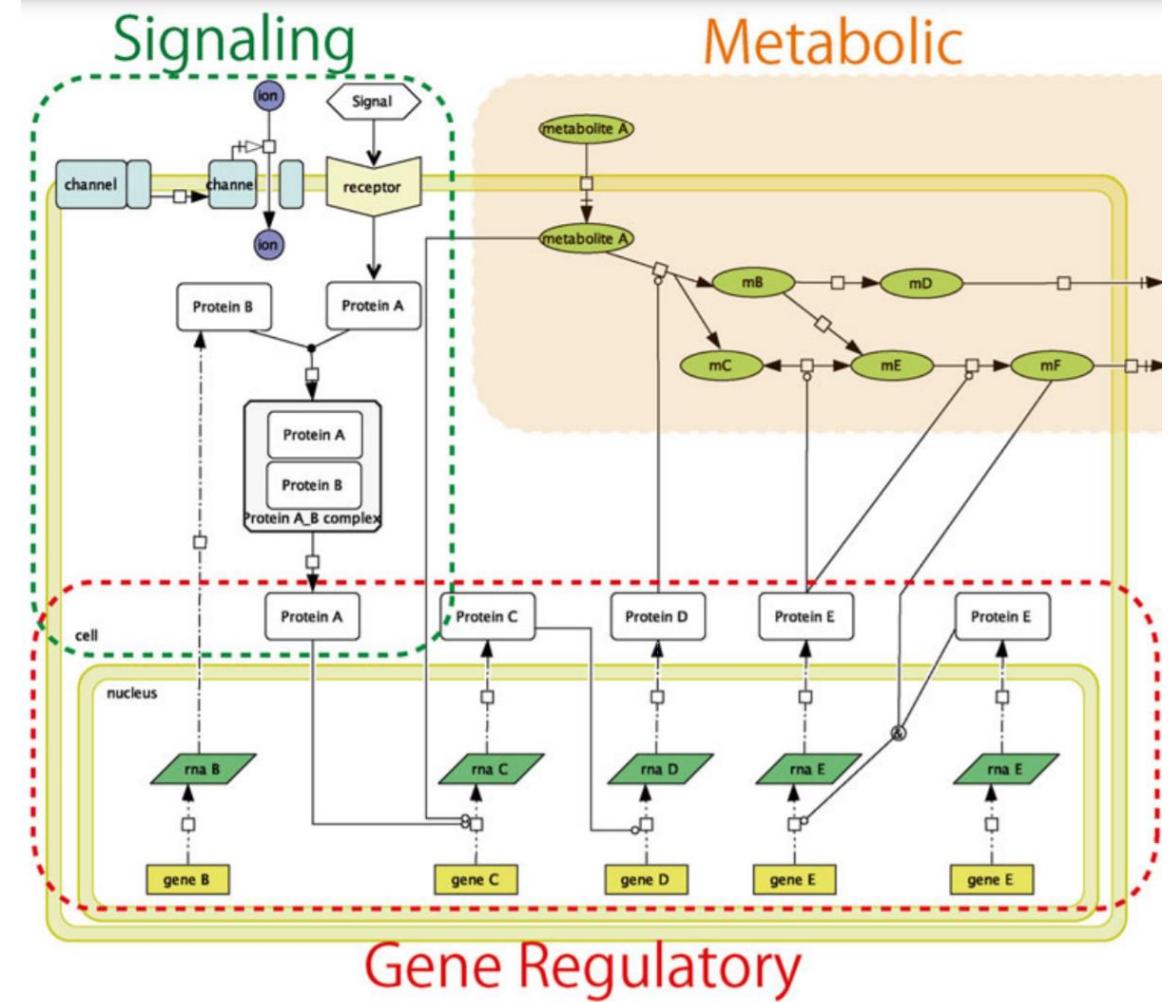


Fig. 1 Signaling/gene regulatory/metabolic pathways captured in a model created by CellDesigner

CellDesigner content



Full SBML support



Graphical notation (SBGN)



Possibility for mathematical simulations



Database connection



Export to PDF, PNG, ...



Freely available



Supported Environment

Windows

Mac OS X

Linux

What is CellDesigner good for?



CellDesigner:



Offers an « easy-to-use » graphical representation of a network



Facilitates exchange of models developed by different groups, using a standard language (SBML: Systems Biology Markup Language)



Allows to annotate the reactions, proteins, genes, etc.



Proposes links to other databases (PubMed, IHOP, BioModels, KEGG, etc.)



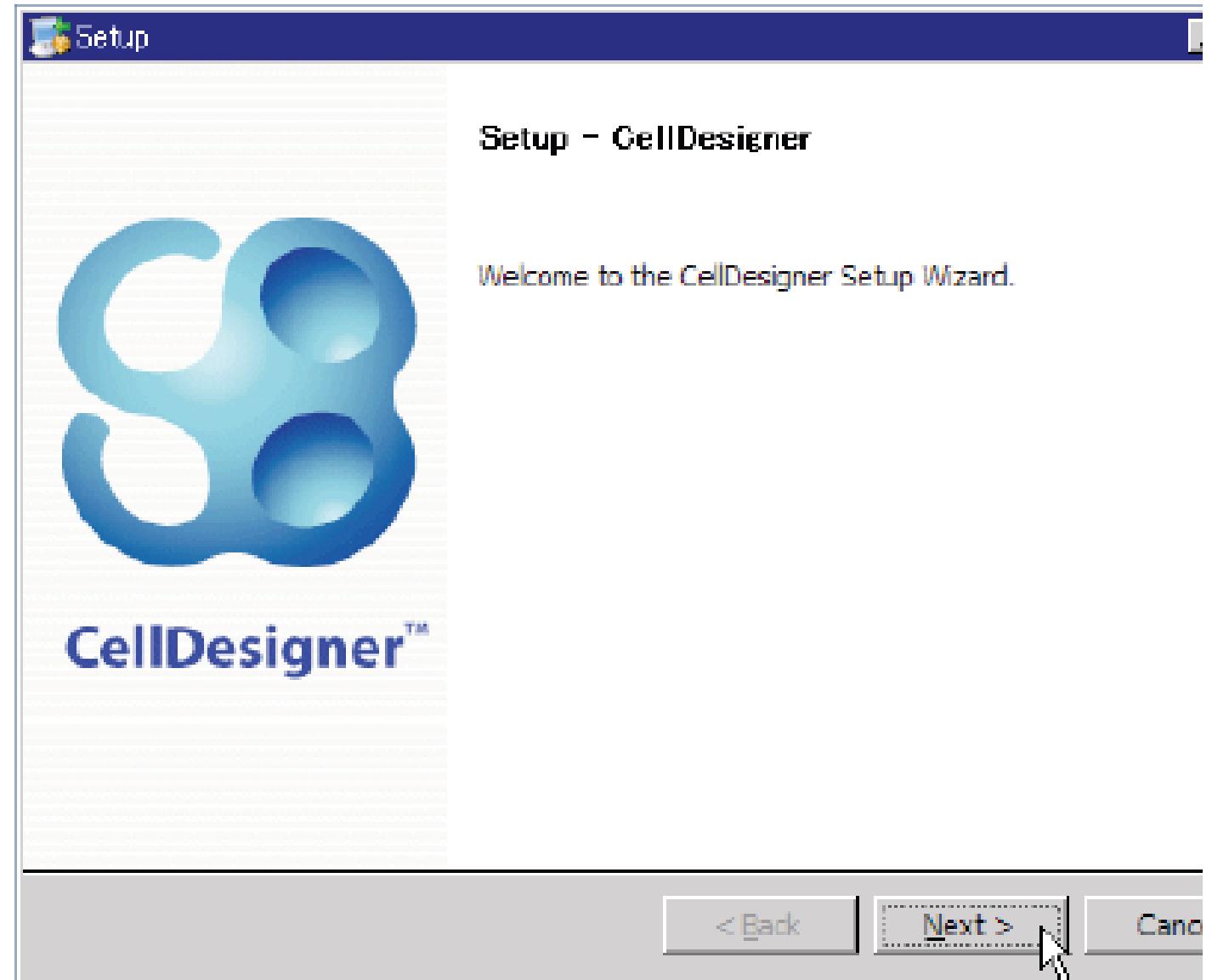
Organizes a lot of information in a unique diagram



Allows an exchange with other modeling tools

Install and Start CellDesigner

Download CellDesigner version 4.2.2
from <http://celldesigner.org>



General view

TREE AREA

displays all the list of the components in a tree structure.

DRAW AREA

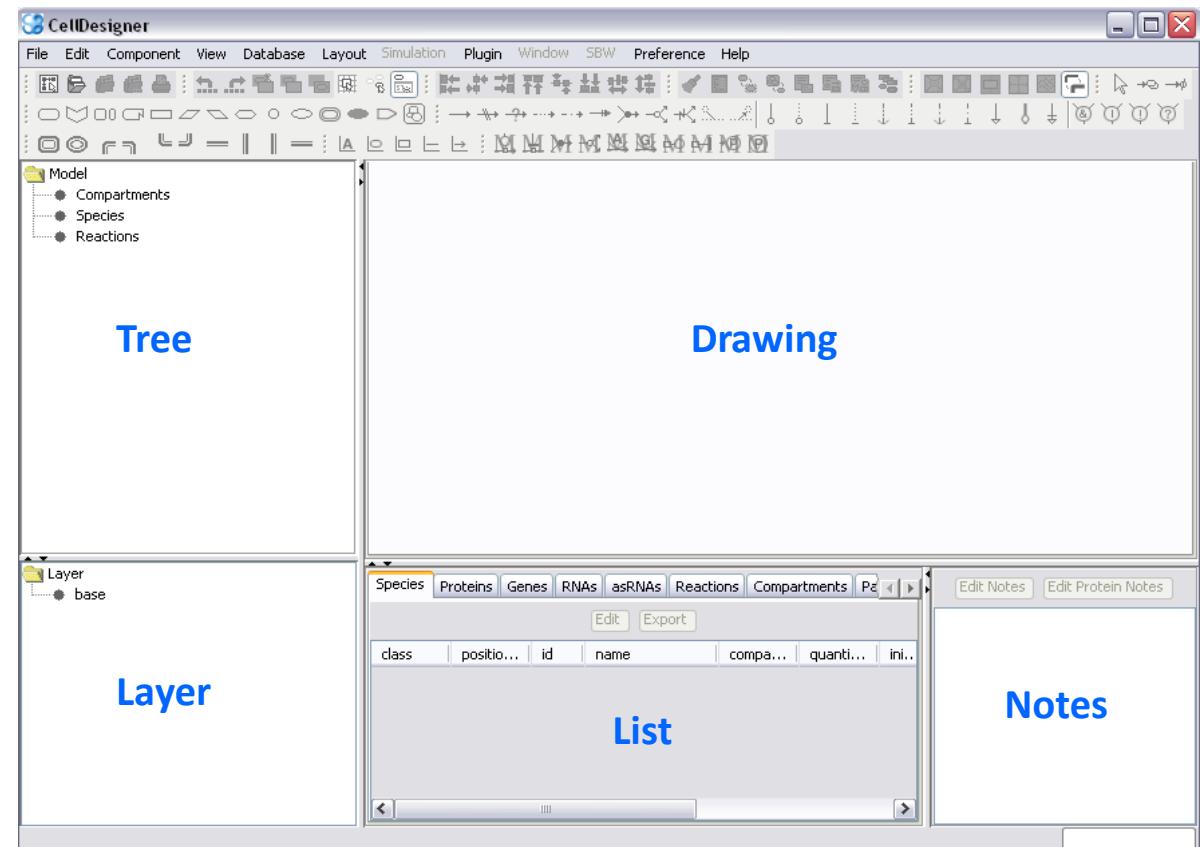
is the area where the model is built from the tool bar items.

LIST AREA

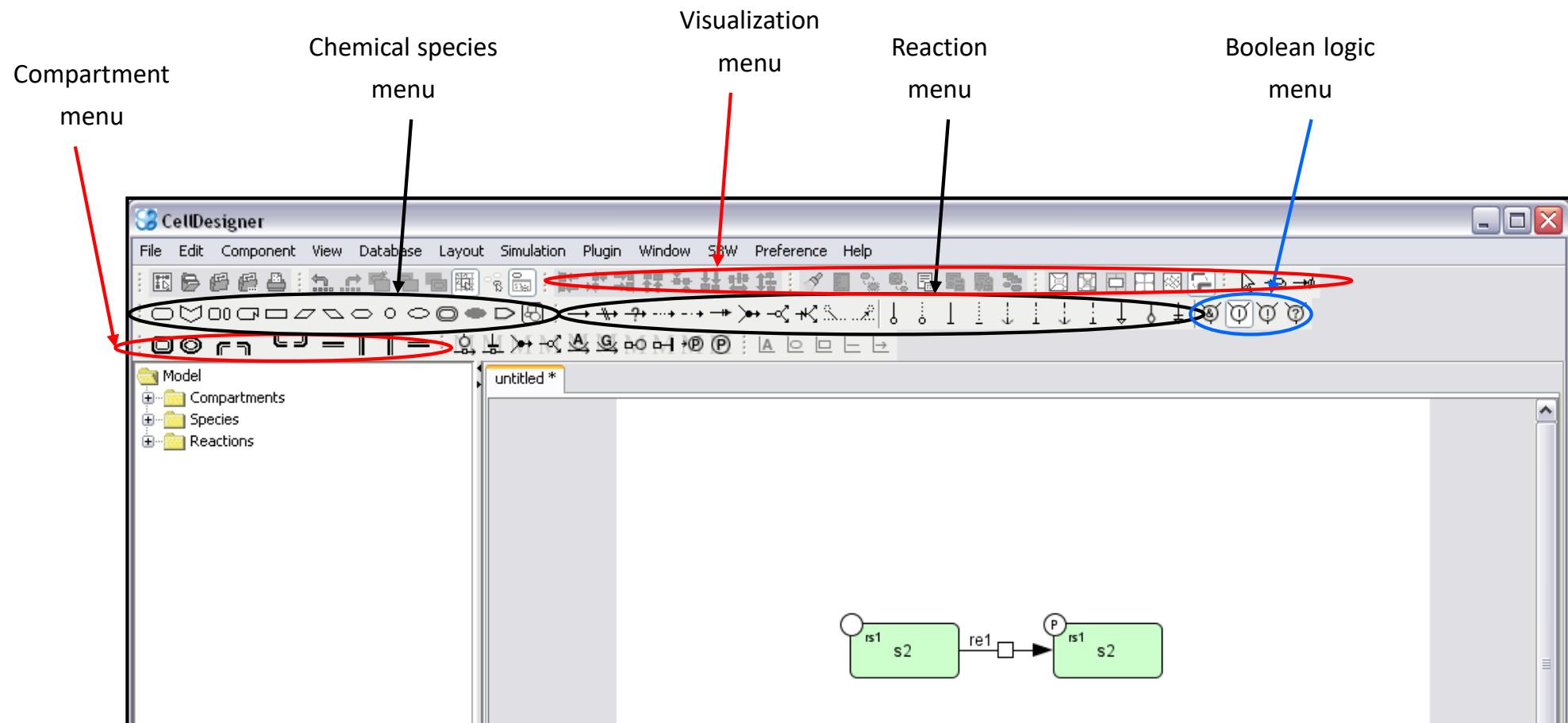
displays and edits the list of the components of the model (species, proteins, genes, RNAs, etc.)

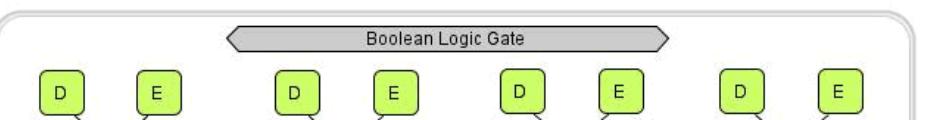
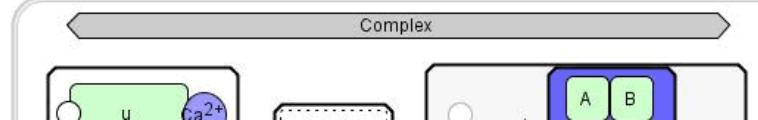
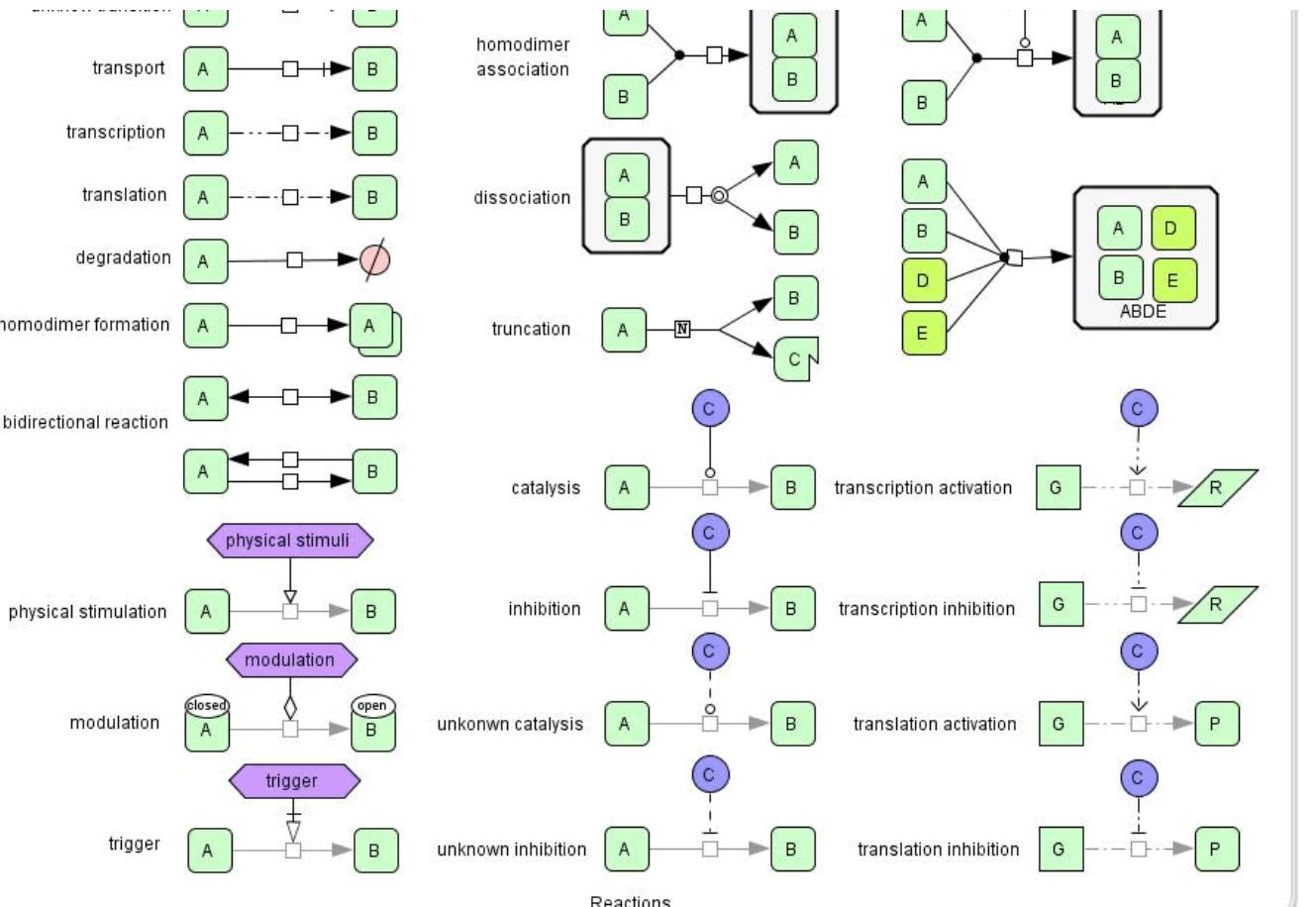
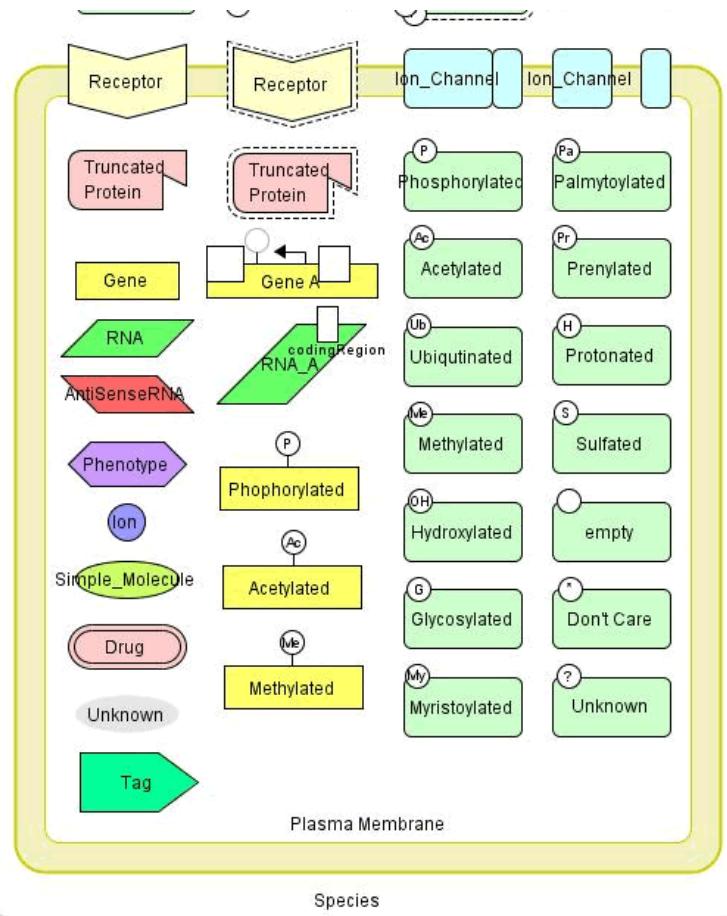
NOTES AREA

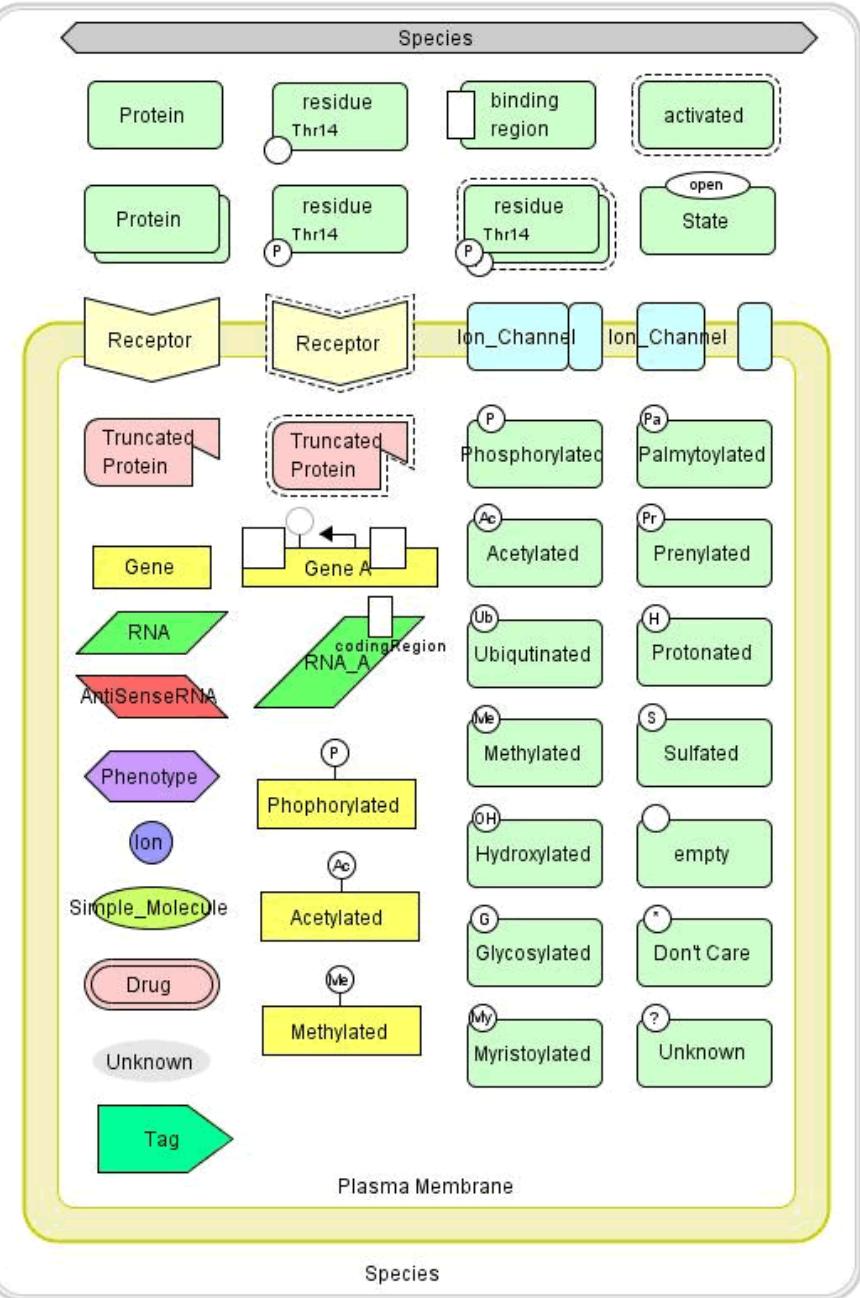
displays and edits the notes of each component (reactions, protein, complex, etc.)



The menu







Modeling and Simulation Using CellDesigne

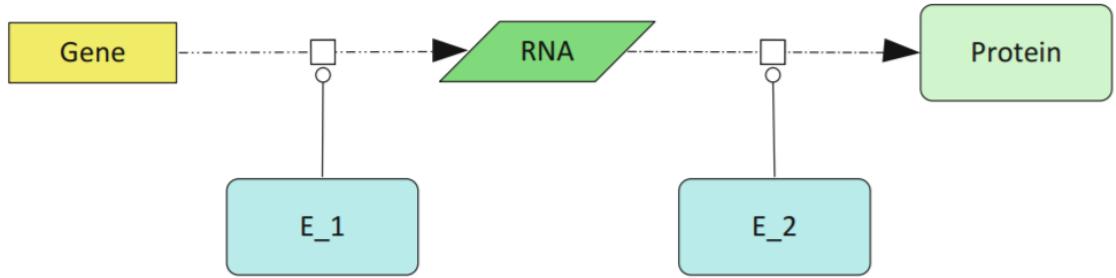
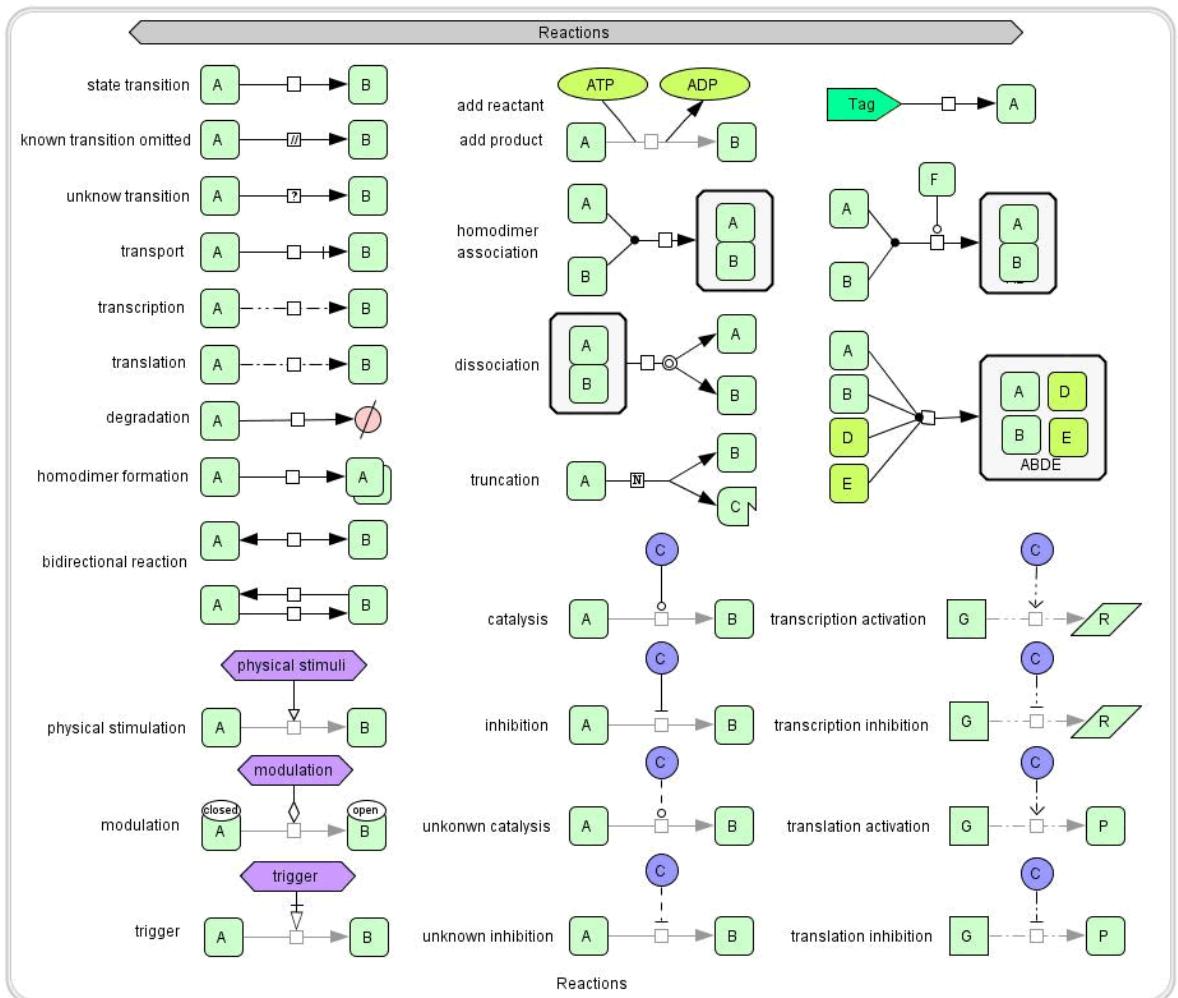


Fig. 4 An example of synthesis of a protein

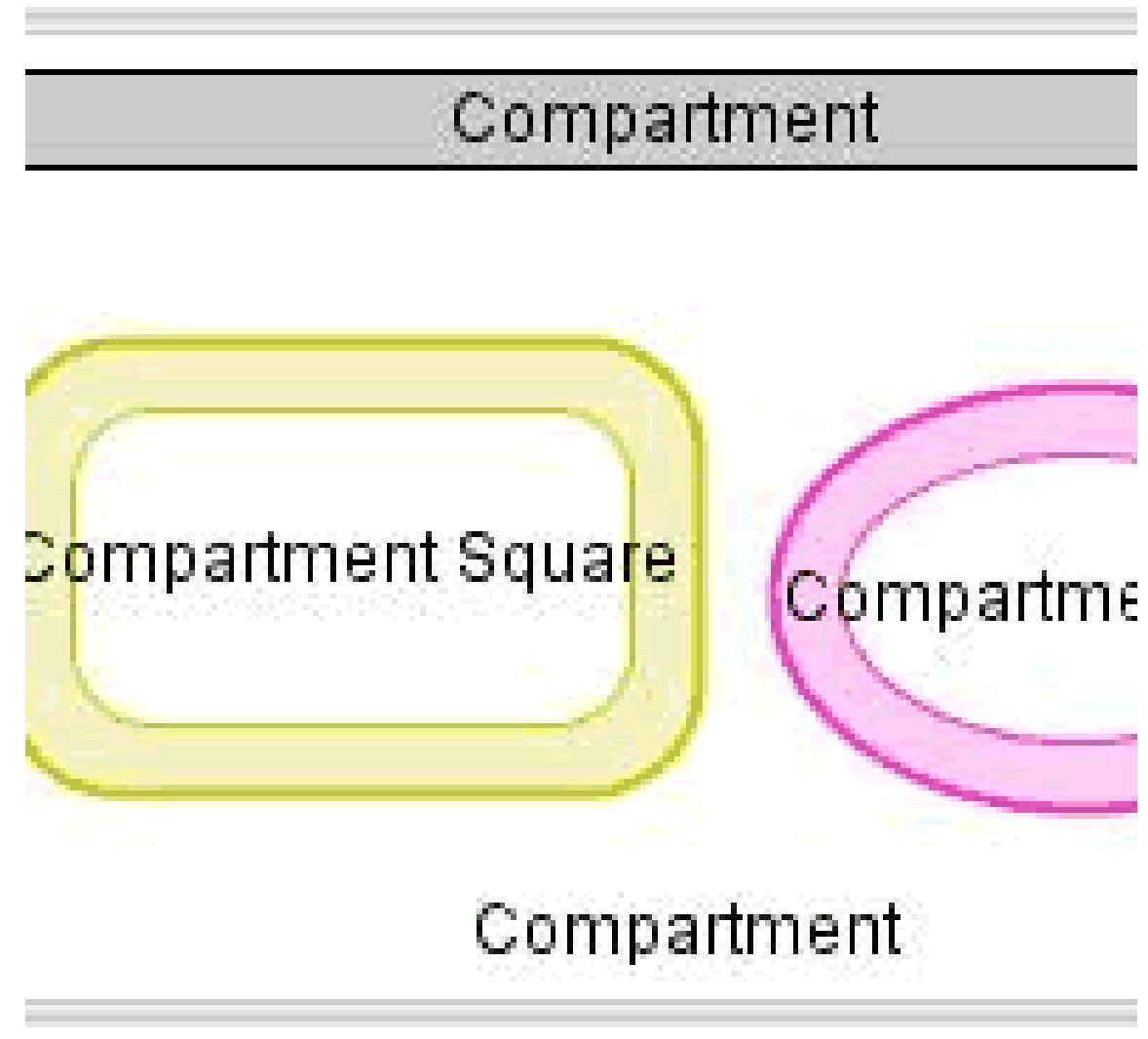
The chemical species

The reactions

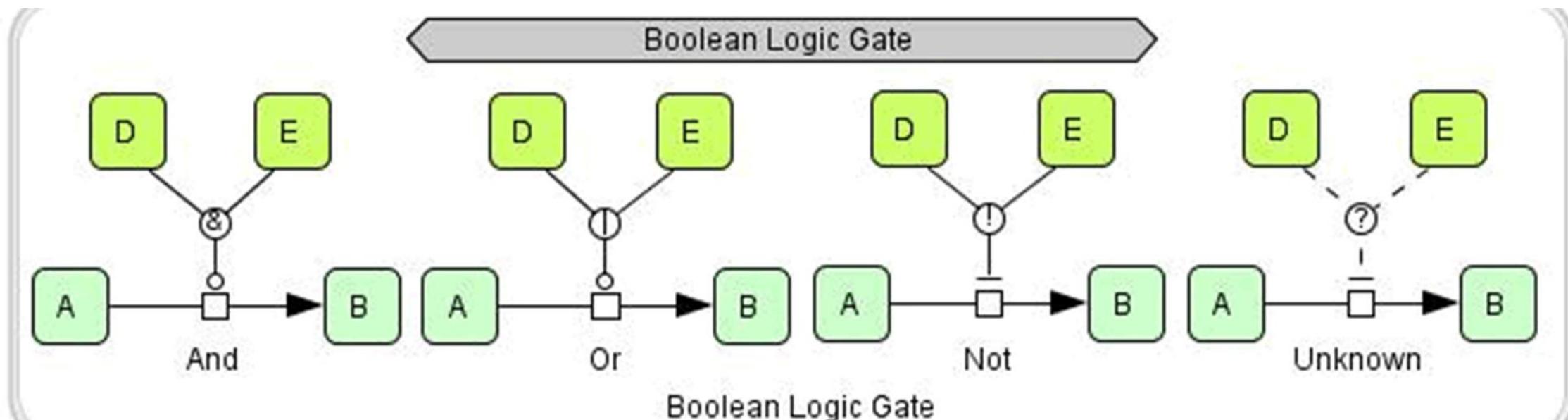


The compartments

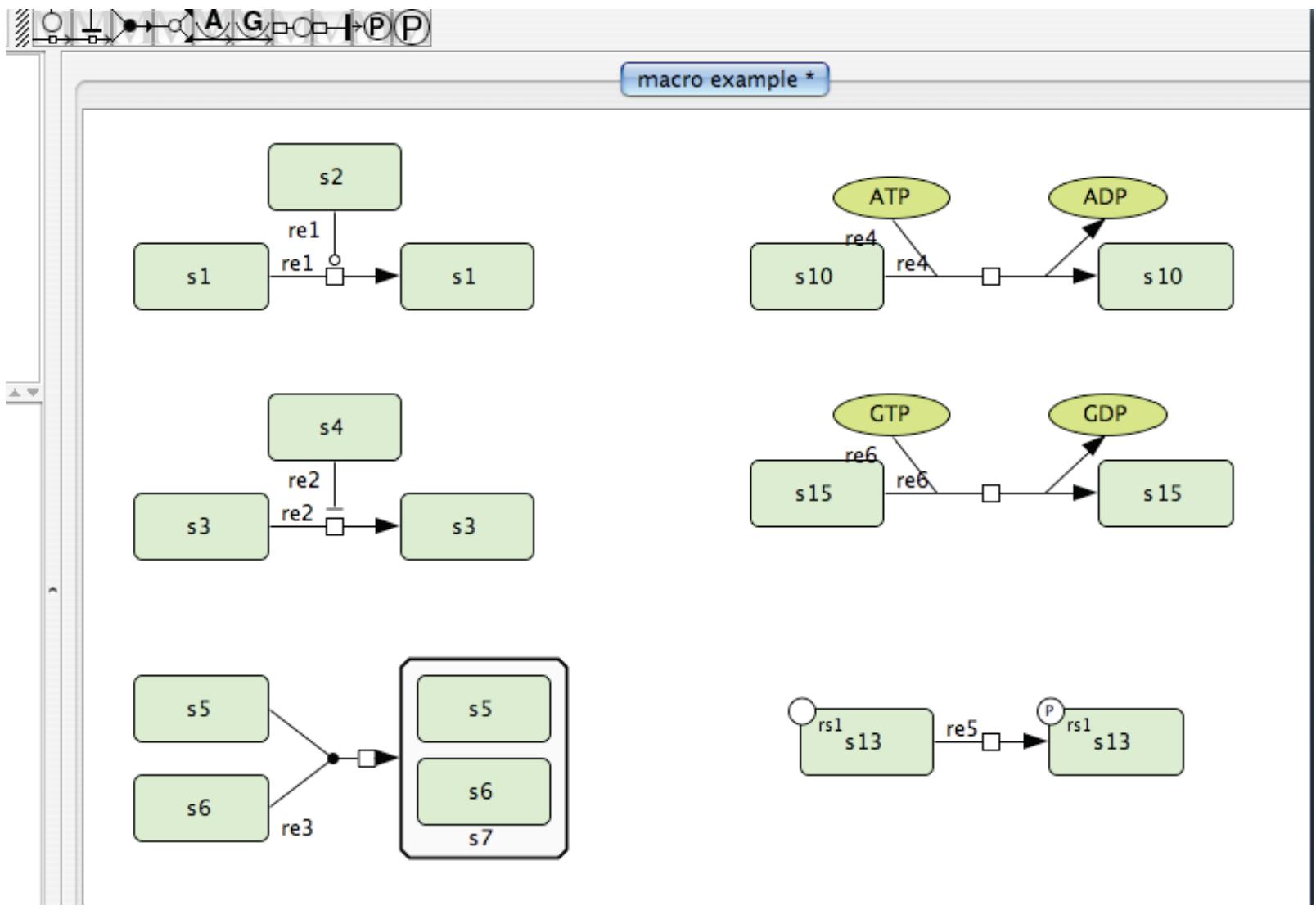
- Compartments can be:
- Cytoplasm
- Nucleus
- Nucleolus
- etc.



Boolean gates



Introduce boolean logic information into the diagram



Examples of
macros

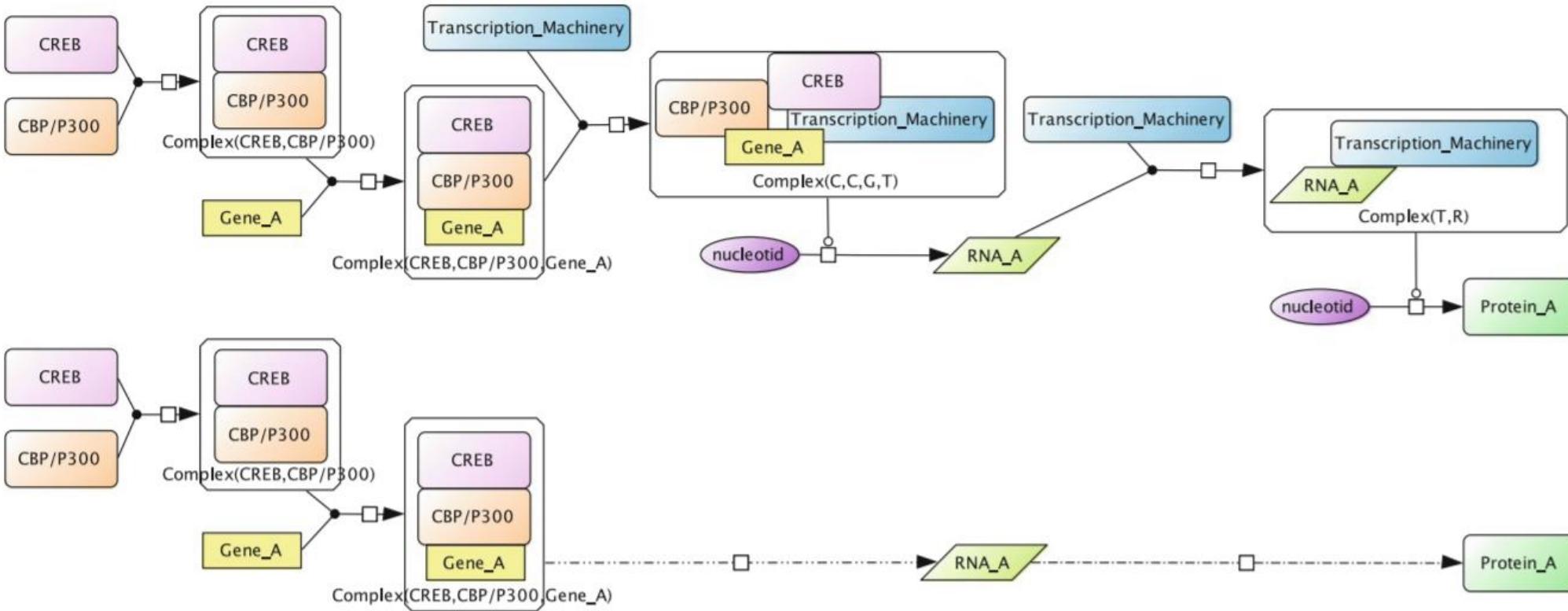


Fig. 5 An example of transcription and translation diagram (CellDesigner sample file: Sample/nbt/CD4.1/SuplFig4a_TranscriptionTranslation_4.xml) [30]

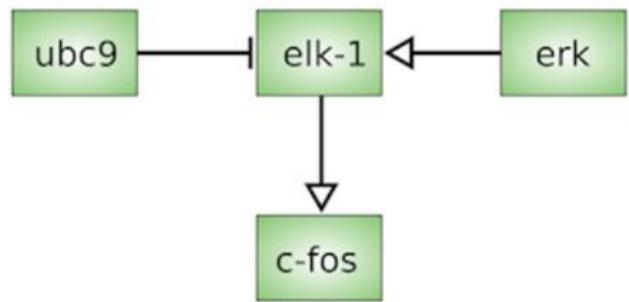


<https://sbgn.github.io/>



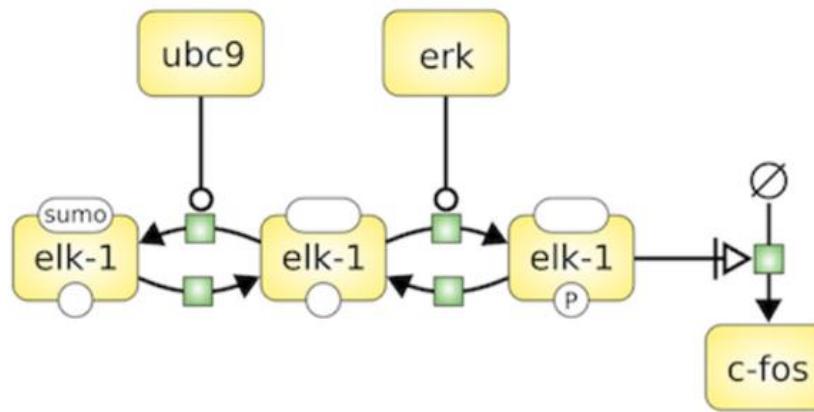
[WHAT IS SBGN](#)
[SPECIFICATIONS](#)
[SOFTWARE](#)
[EVENTS](#)
[FAQ](#)
[HOW TO CITE](#)
[ABOUT](#)
[CONTACT](#)

activity flows



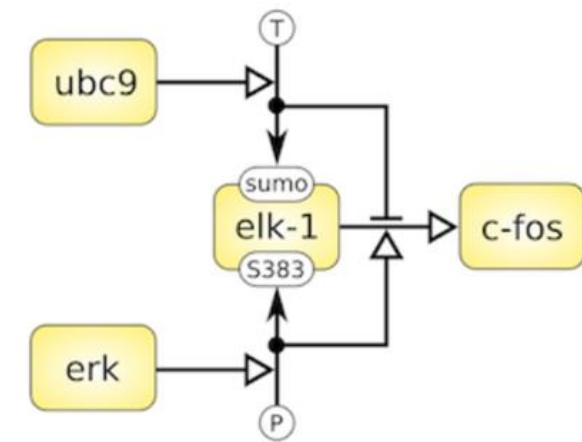
directed
sequential
mechanistic

process descriptions



directed
sequential
mechanistic

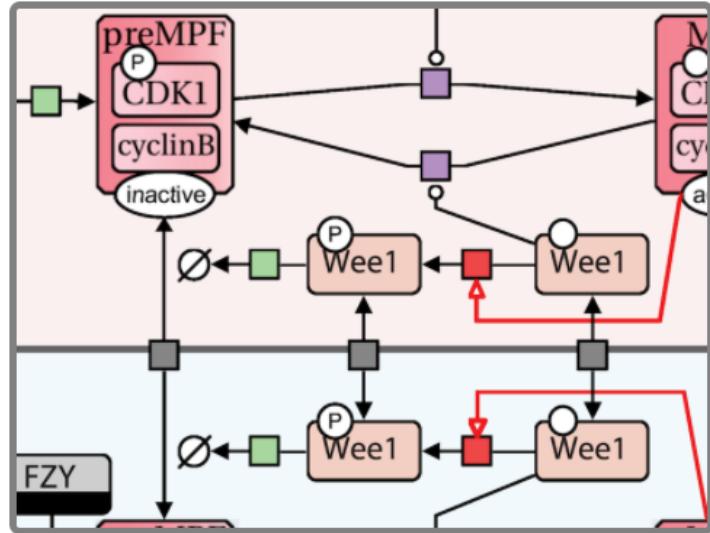
entity relationships



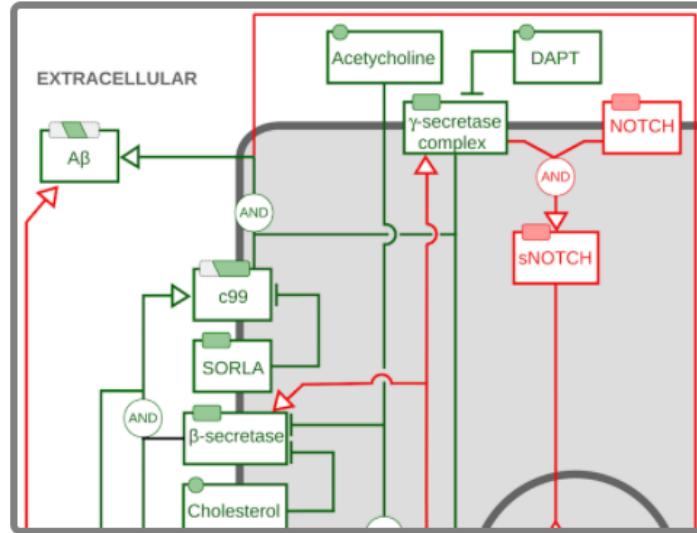
directed
sequential
mechanistic

Cool visualization

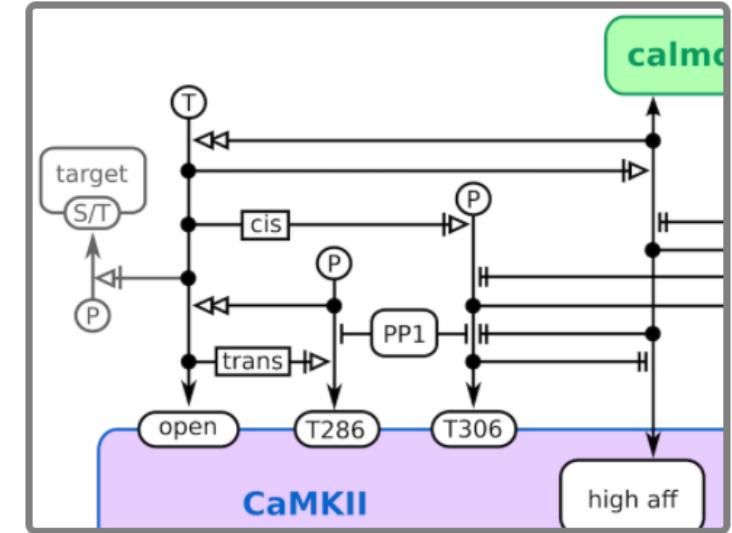
PD map of the Drosophila cell cycle,
[doi:10.1371/journal.pcbi.1005740](https://doi.org/10.1371/journal.pcbi.1005740)



AF map of protein precursor processing,
[doi:10.1002/psp4.12155](https://doi.org/10.1002/psp4.12155)



ER map of CaMKII regulation by calmodulin,
[doi:10.1371/journal.pone.0029406](https://doi.org/10.1371/journal.pone.0029406)

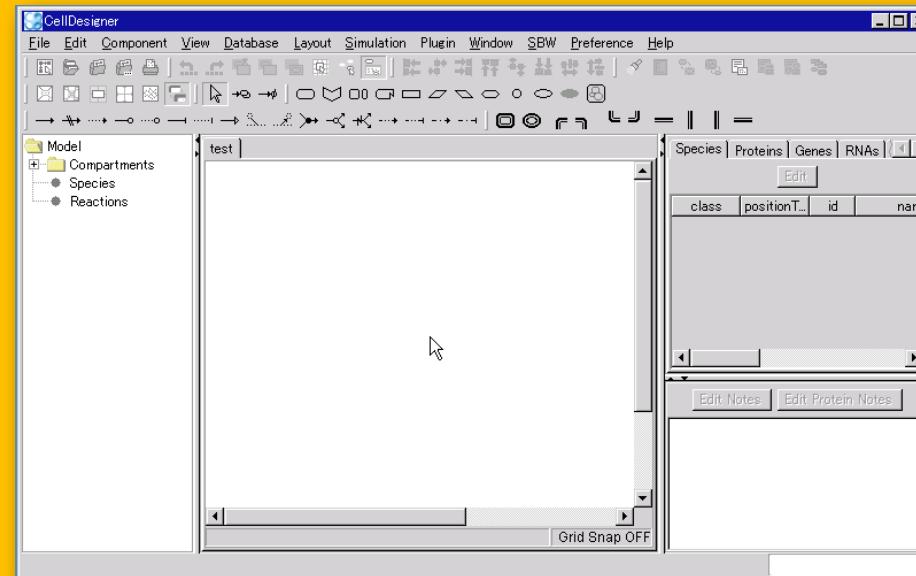
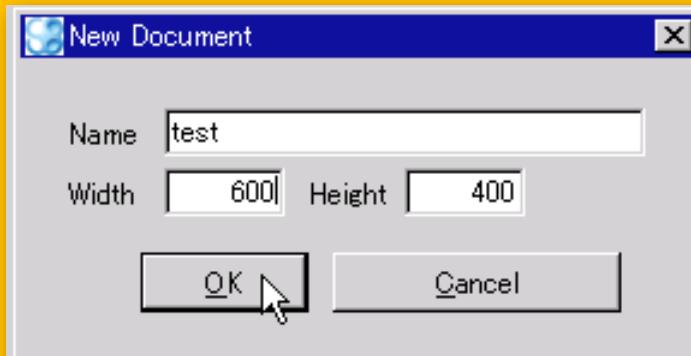
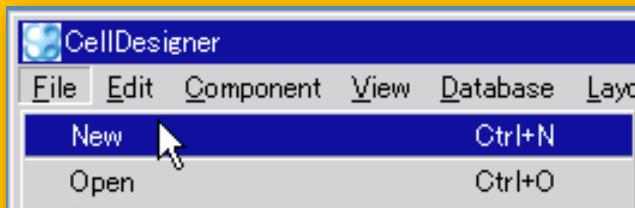


Standard notation schemes

Demonstration

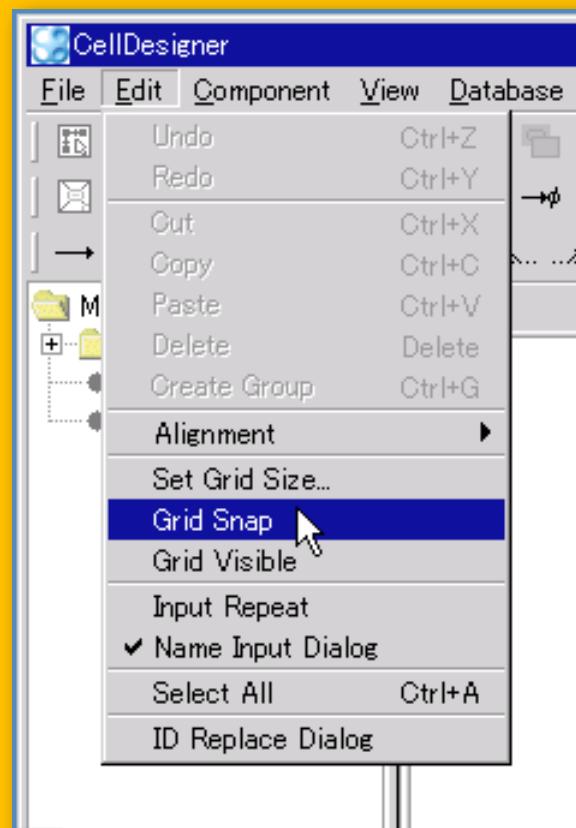
● Create new model:

● [File] → [New] → input title → [OK]



Tips

- Enable [Grid Snap] will help you draw your model much easier



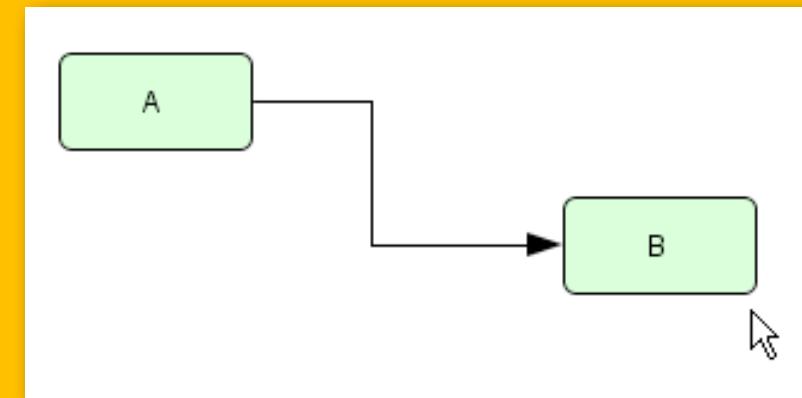
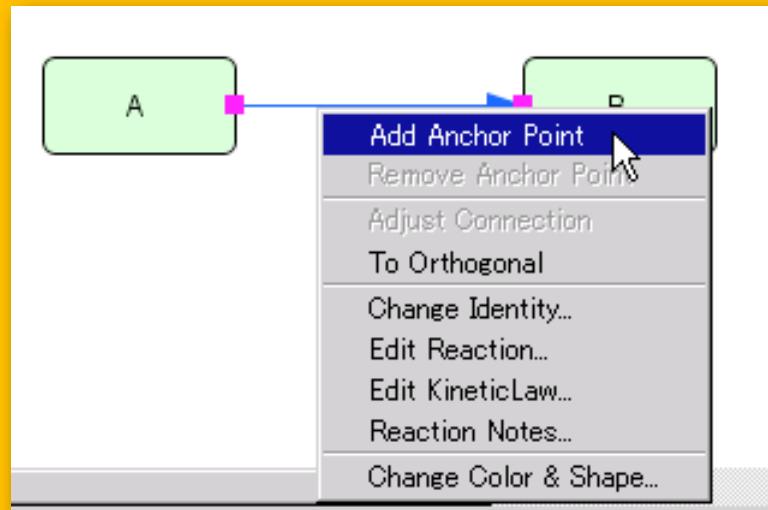
Create Reaction

- Create Protein “A” and “B”
- Draw “State transition” arrow from “A” to “B”



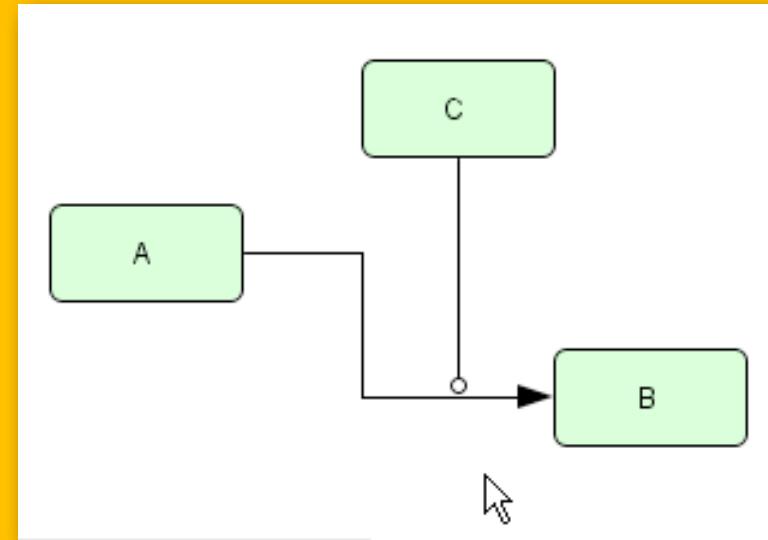
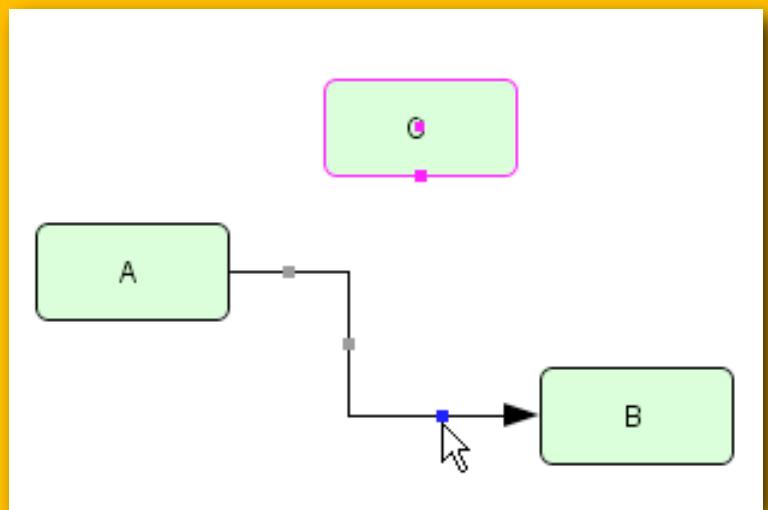
Add Anchor Point

- Add 2 anchor points to reaction
- Drag reaction and anchor point to change its shape



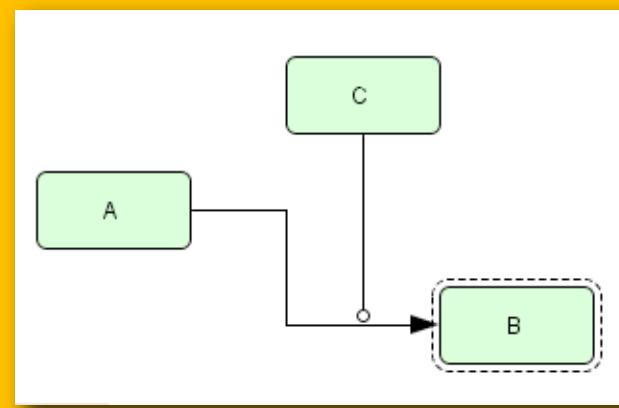
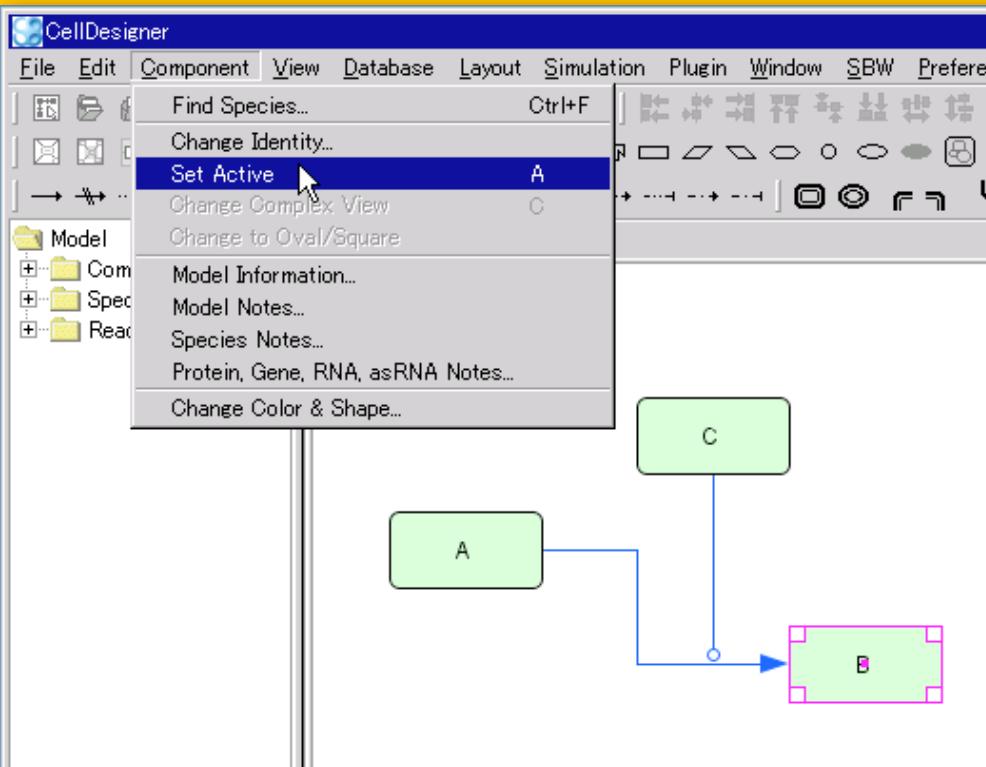
Add Catalysis reaction

- Add Protein “C”
- Add Catalysis reaction from “C” to the reaction



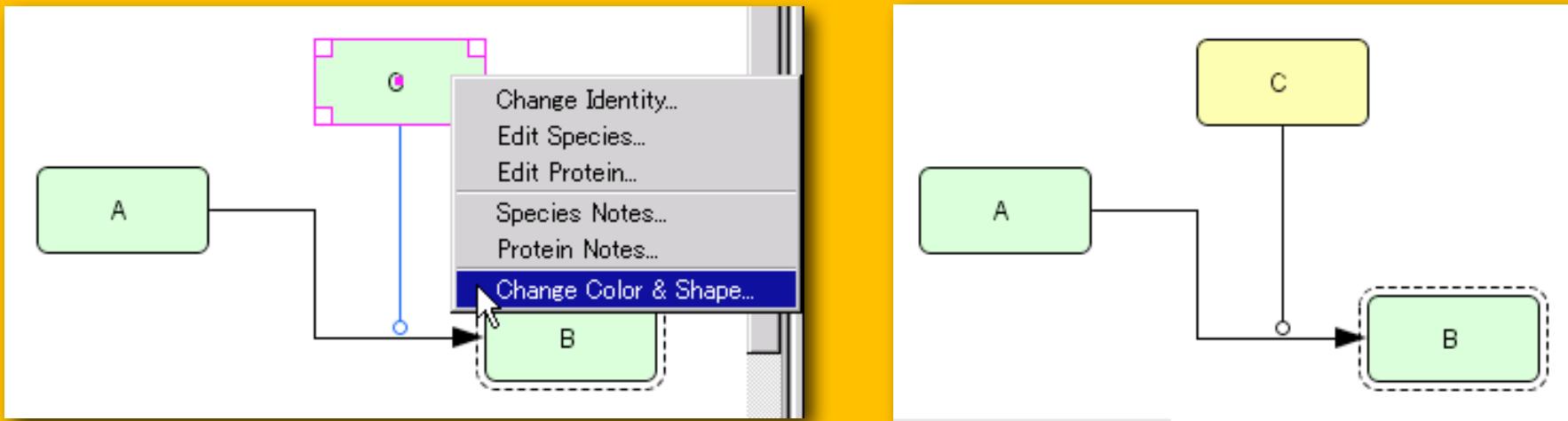
Set Active state

- Select Protein “B”
- [Component] → [Set Active]



Change Color

- Right click on Protein “C”
- Select [Change Color & Shape...]

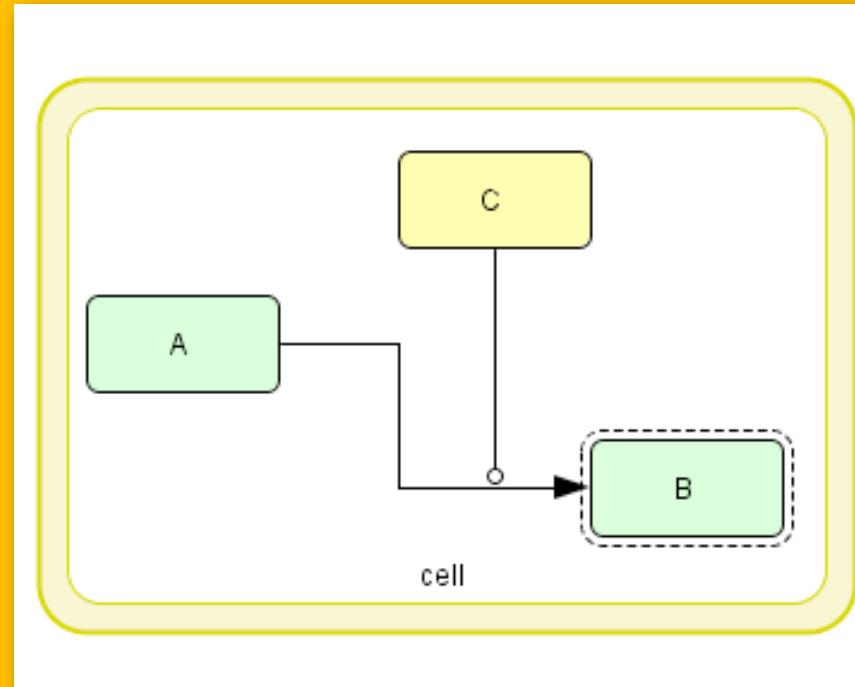


Compartment

- Click [Compartment] icon

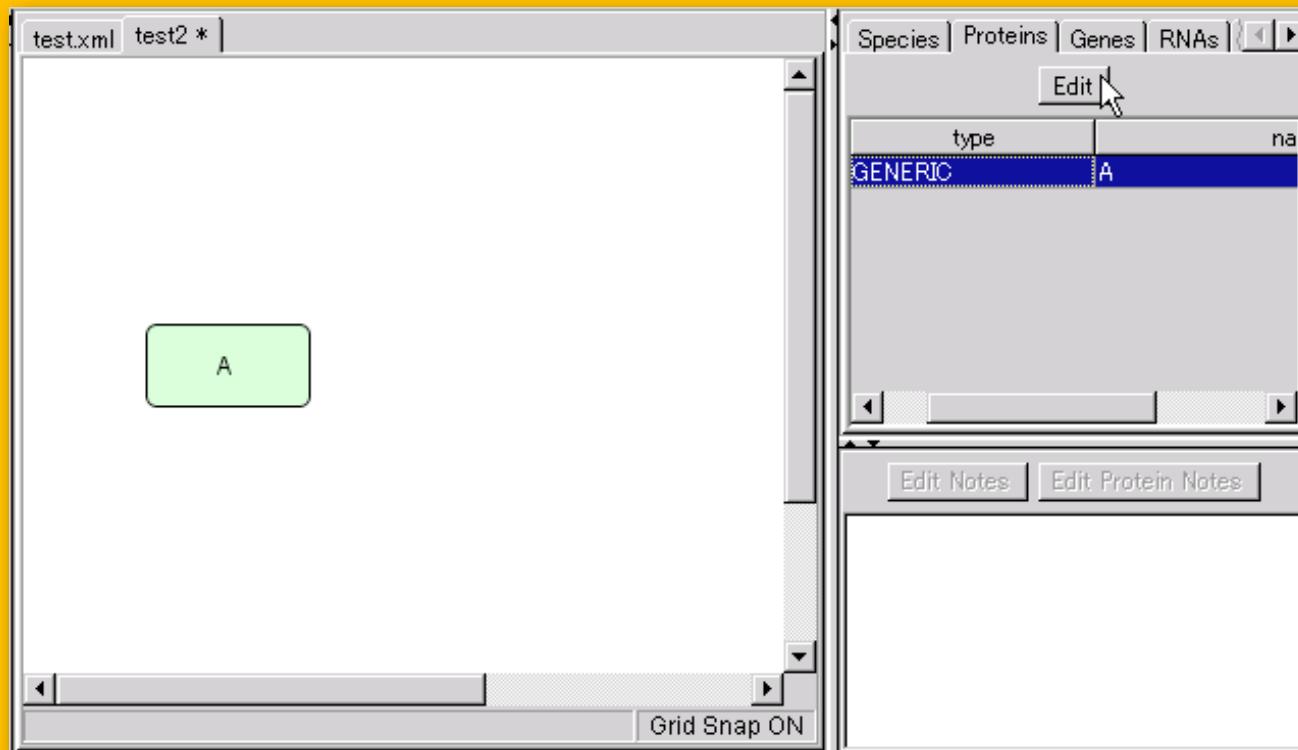


- Drag mouse cursor to specify its area
- Input name of compartment



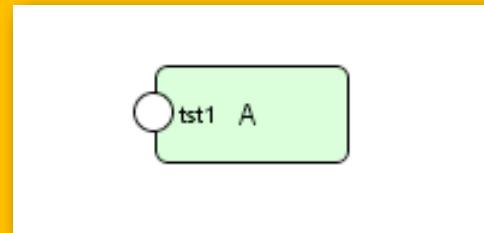
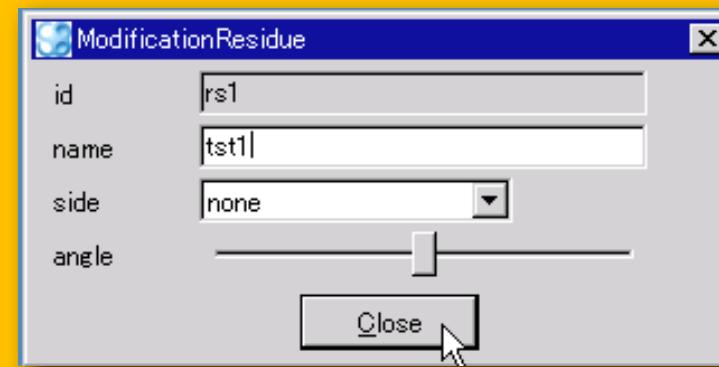
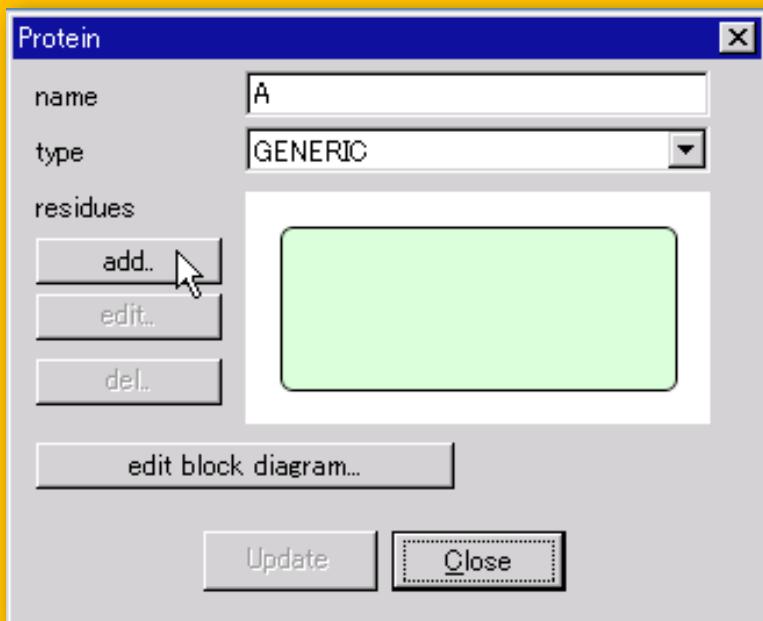
Add Residue to Protein

- Create new model (test2)
- Create Protein “A”
- Select Protein “A” in [Proteins] Tab
- Click [Edit] button



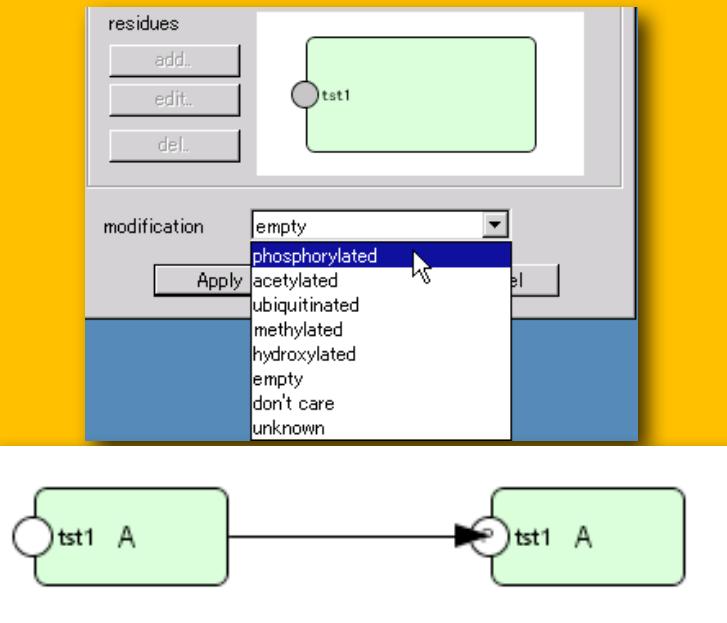
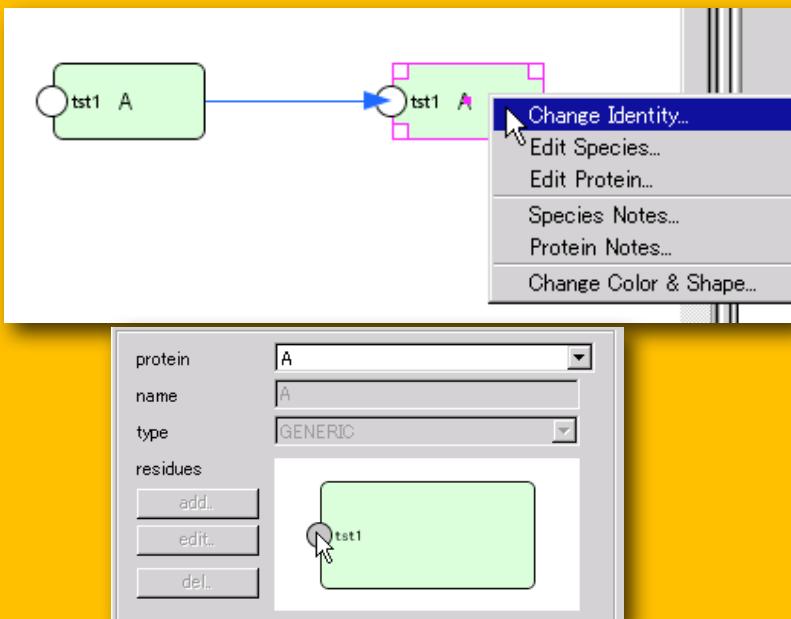
Add Residue to Protein

- Click [add] button on [Protein] dialog
- Input name for the residue (tst1)
- Click [Close] button
- Click [Update] Button



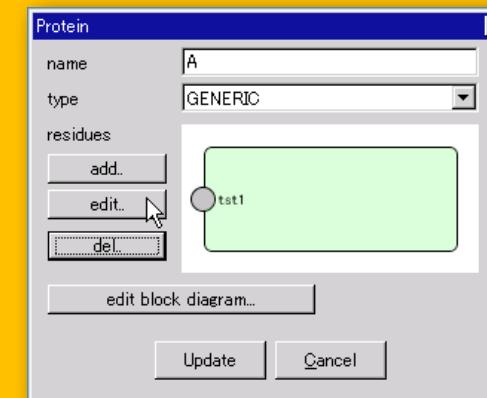
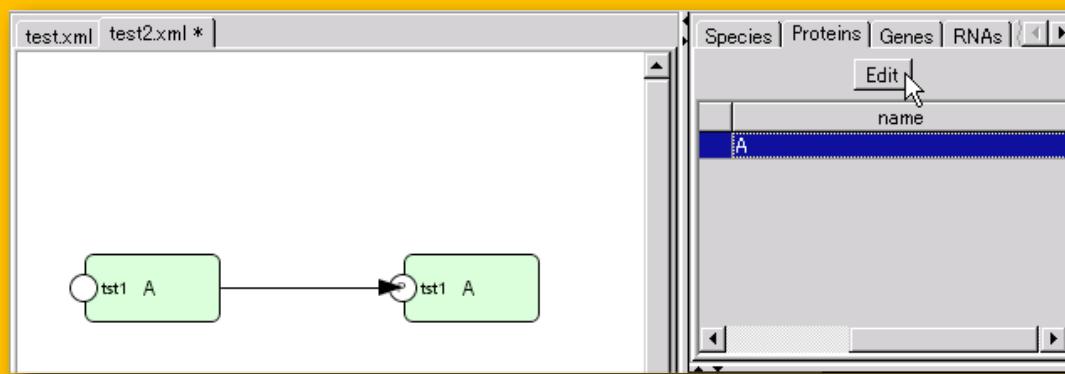
Add Residue to Protein

- Copy & Paste Protein “A” and then draw “State Transition” arrow
- Right Click on “A” (right side) and select [Change Identity...]
- Click residue “tst1” in Dialog
- Select [phosphorylated] in modification



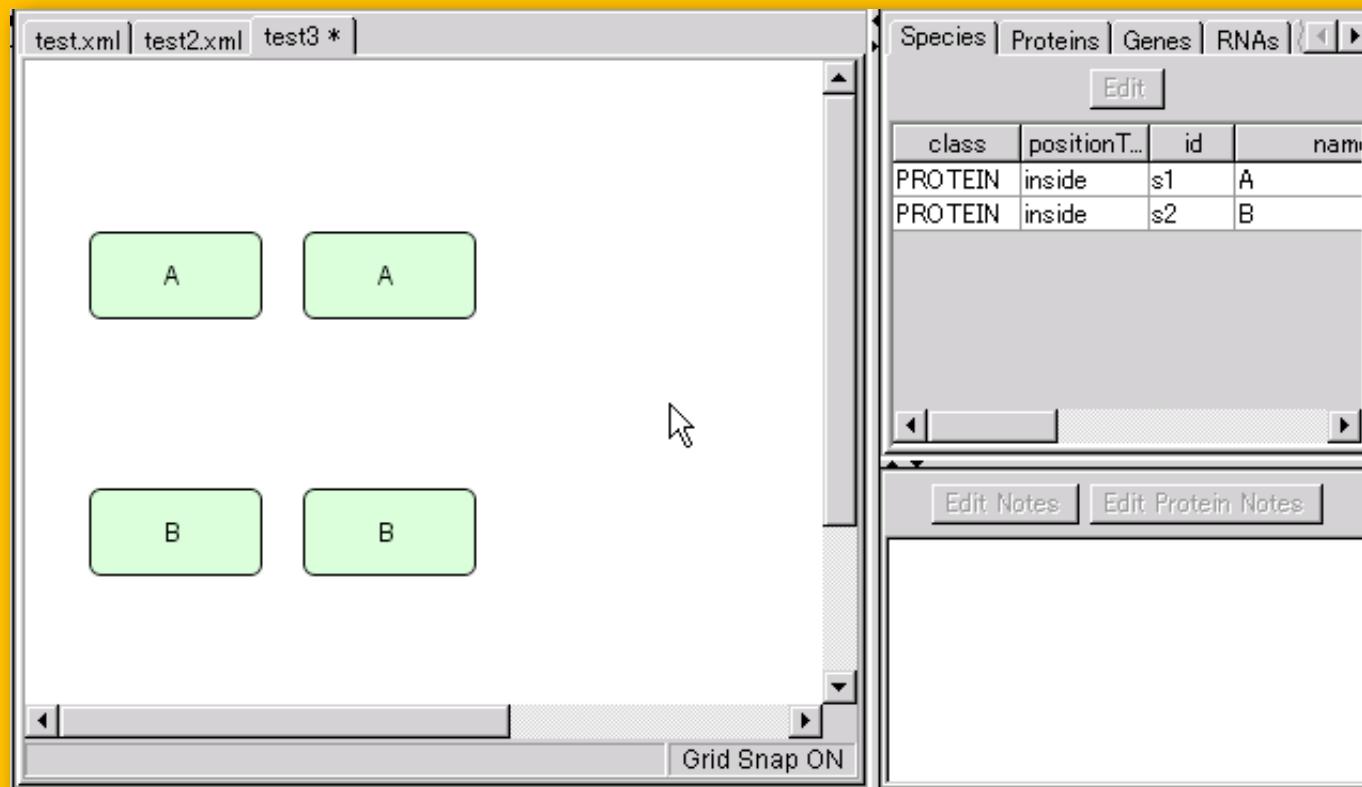
Change position of Residue

- Select Protein “A” in [Proteins] Tab
- Click [Edit] button
- Click residue “tst1” in Dialog
- Click [edit] button
- Drag [angle] sidebar



Complex

- Create new model (test3)
- Create Proteins “A” and “B”
- Copy & Paste both “A” and “B”

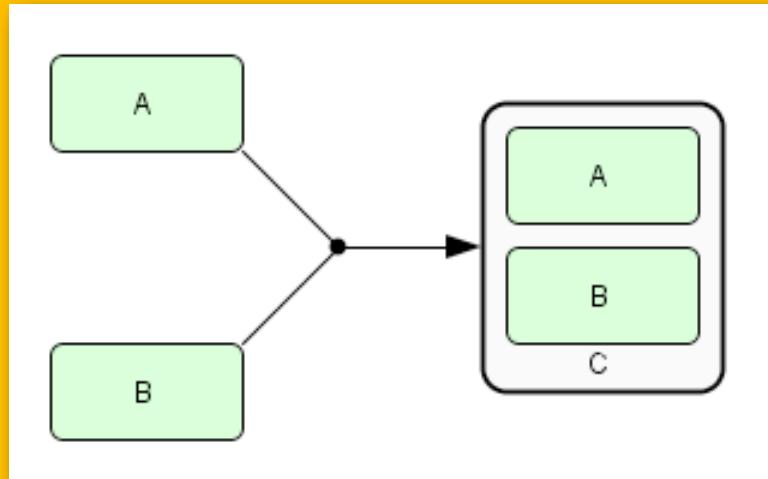


Complex

- Click [Complex] icon and create complex “C”

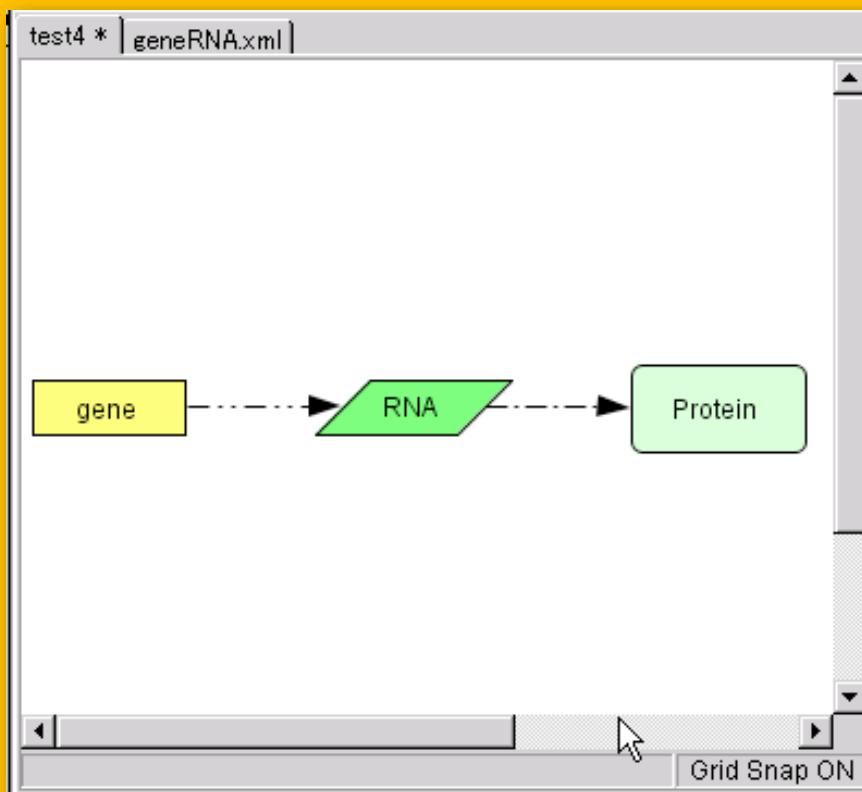


- Drag Protein “A” and “B” into complex C
- Draw “Association” arrow



Gene & RNA

- Create new model (test4)
- Create gene, RNA and Protein
- Draw “Transcription” and “Translation”



Database Connection

Import model from
BioModels.net

The screenshot shows the CellDesigner interface with a context menu open over a model. The menu is titled 'Import model from BioModels.net...' and includes options like 'Connect to SGD', 'Connect to DBGET', 'Connect to iHOP', 'Connect to Genome Network Platform', 'Connect to PubMed', and 'Connect to Entrez Gene'. Below the menu is a list of BioModels.net entries, with one entry highlighted.

ID	Name
BIOMD0000000001	Edelstein1996 - EPSP ACh event
BIOMD0000000002	Edelstein1996 - EPSP ACh species
BIOMD0000000003	Goldbeter1991 - Min Mit Oscil
BIOMD0000000004	Goldbeter1991 - Min Mit Oscil, Expl Inact
BIOMD0000000005	Tyson1991 - Cell Cycle 6 var
BIOMD0000000006	Tyson1991 - Cell Cycle 2 var
BIOMD0000000007	Novak1997 - Cell Cycle
BIOMD0000000008	Gardner1998 - Cell Cycle Goldbeter
BIOMD0000000009	Huang1996 - Ultrasensitivity in MAPK cascade
BIOMD0000000010	Kholodenko2000 - Ultrasensitivity and negative feedback bring...
BIOMD0000000011	Levchenko2000_MAPK_noScaffold
BIOMD0000000012	Elowitz2000 - Repressilator
BIOMD0000000013	Poolman2004_CalvinCycle
BIOMD0000000014	Levchenko2000_MAPK_Scaffold
BIOMD0000000015	Curto1998 - purine metabolism
BIOMD0000000016	Goldbeter1995_CircClock
BIOMD0000000017	Hoefnagel2002_PyruvateBranches
BIOMD0000000018	Morrison1989 - Folate Cycle
BIOMD0000000019	Schoeberl2002 - EGF MAPK
BIOMD0000000020	hodgkin-huxley squid-axon 1952
BIOMD0000000021	Leloup1999_CircClock
BIOMD0000000022	Ueda2001_CircClock
BIOMD0000000023	Rohwer2001_Sucrose
BIOMD0000000024	Scheper1999_CircClock
BIOMD0000000025	Smolen2002_CircClock

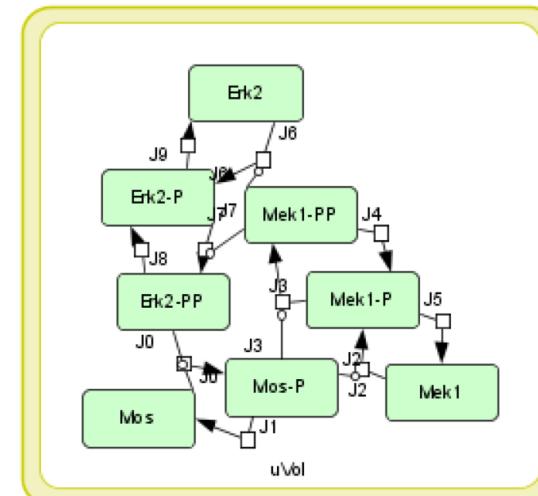
Buttons at the bottom of the dialog include 'Description', 'Reference', 'Import' (highlighted in blue), and 'Cancel'.



Model

- Compartments
- Species
- Reactions

BIOMD0000000010



layer
● base

Grid Snap OFF

Species	Proteins	Genes	RNAs	asRNAs	Reactions	Compartments	Parameters	Functions	UnitDefinitions	Rules	Events	SpeciesTypes	Compartme...
Edit Export													
class	id	name	speciesType	compar...	position...	included	quantit...	initialQuantity	sub...	hasO...	b.c.	c...	
PROTEIN	MKKK	Mos		uVol	transme...		Concentr...	90.0		false	false	false	
PROTEIN	MKK...	Mos-P		uVol	transme...		Concentr...	10.0		false	false	false	
PROTEIN	MKK	Mek1		uVol	transme...		Concentr...	280.0		false	false	false	
PROTEIN	MKK_P	Mek1-P		uVol	transme...		Concentr...	10.0		false	false	false	
PROTEIN	MKK...	Mek1-PP		uVol	transme...		Concentr...	10.0		false	false	false	
PROTEIN	MAPK	Erk2		uVol	transme...		Concentr...	280.0		false	false	false	

NOTE MIRIAM

Edit Notes Edit Protein Notes

CellDesigner

File Edit Component View Database Layout Simulation Plugin Window SBW Garuda Preference Help



Model
+ Compartments
Species
Reactions

Layer
base

BIOMD0000000010 interleukin

Name of the species



IL6

OK

Cancel

Grid Snap OFF

Species	Proteins	Genes	RNAs	asRNAs	Reactions	Compartments	Parameters	Functions	UnitDefinitions	Rules	Events	SpeciesTypes	Compartme...	Edit	Export
class	id	name			speciesType	compar...	position...	included		quantit...	initialQuantity	sub...	hasO...	b.c.	c...

NOTE MIRIAM
Edit Notes Edit Protein Notes

Database -> connect to Entrez Gene

NCBI Resources How To Sign in to NCBI

Gene Gene IL6 Search Create RSS Save search Advanced Help

COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: <https://www.coronavirus.gov>.
Get the latest research from NIH: <https://www.nih.gov/coronavirus>.
Find NCBI SARS-CoV-2 literature, sequence, and clinical content: <https://www.ncbi.nlm.nih.gov/sars-cov-2/>.

Gene sources Tabular 20 per page Sort by Relevance Send to: Hide sidebar >>

Categories

- Alternatively spliced
- Annotated genes
- Non-coding
- Protein-coding

Sequence content

- CCDS
- Ensembl
- RefSeq
- RefSeqGene

Status clear

Current

Clear all Show additional filters

Filters: [Manage Filters](#)

Results by taxon

Top Organisms [Tree]

- Homo sapiens (258)
- Mus musculus (86)
- Rattus norvegicus (26)
- Bos taurus (22)
- Tupaia chinensis (9)
- All other taxa (559)

More...

Find related data

Database: Select Find items

GENE Was this helpful?  

IL6 – interleukin 6

Homo sapiens (human)

Also known as: BSF-2, BSF2, CDF, HGF, HSF, IFN-beta-2, IFNB2, IL-6

GenID: 3569

[RefSeq transcripts](#) (5) [RefSeq proteins](#) (5) [RefSeqGene](#) (1) [PubMed](#) (4,649)

Orthologs Genome Browser BLAST Download

Inventory of features

Open a new model

Create a reaction

Add anchor point

Add catalytic reaction

Set active state

Change color

Include compartment

Add residue to protein

Change position of residue

Create complex

Include genes and RNAs

Connect to databases

Choose layout

<http://www.Celldesigner.Org/>

Documents Help Model Repository Forum Plugins News Links Contacts

Help - Home > Quick Tutorial

Quick Tutorial

- Getting to Know CellDesigner
 - Starting the program
 - Navigation
- Creating a new Model
 - Species
 - Add a Protein on the Canvas
 - Add Protein Residues
 - Change the Residue/Region Status
 - Create Reaction
 - Tidy up your diagram layout
 - Export Images / Print Images
 - Customizing Properties
 - Add Notes (e.g. literature references) and MIRIAM to Proteins/Reactions
 - Refer to the databases
- Running the simulation
 - Set the Kinetic Laws / Parameters
 - Set the values of the Species
 - Using Control Panel for simulation
- Import / Export SBML file
- Viewing a Model
 - Connect to Database
 - View Notes

If you are the first-time user we would recommend you to **Guide Ver. 4.3**, which gives instruction using sample files.

Past Tutorial Presentations available:

- ICSB-2010 (Oct 10th,
- ICSB 2009
- Tutorial for Simulation Adams)

CellDesigner.org

ENHANCED BY Google

home | features | downloads | documents | models | forum | news | links | contacts

home

Menu

- Features
- Download
- Quick Tutorial
- Documents
- Help
- Simulation
- Model Repository
- Plugins
- News
- Links

Related Link

systems-biology.org

PANTHER database

BioModels.net

The Systems Biology Institute

Kitano Symbiotic Systems Project

SML

SGN

SBW

CellDesigner™: A modeling tool of biochemical networks

Current Release Version: CellDesigner 4.4.2

macOS Catalina and Ubuntu 18.04 support + Plugin APIs enhances + BioModels new API support + Garuda enabled + bug fixes. find out more...

You do not have to install JVM separately as it is included in the installer.

Check also:

- CellDesigner on Garuda platform (Ver4.4.1 Win / Mac)
- Plugins / Utilities
 - CellDesigner Plugin API Document (ver4.4.1)
- Models built with CellDesigner
- BioModels.net models simulation results with CellDesigner 4.0

What is CellDesigner™



CellDesigner™
Ver. 4.3

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<http://celldesigner.org>

CellDesigner - 4.3.0 - Tue, 29 Feb. 2013

Headlines

CellDesigner 4.4.2 Mac installer updated for Catalina Support (2020/3/30)

CellDesigner 4.4.2 is now available (2019/05/20)

CellDesigner on Garuda platform (2017/2/14) Garuda enabled Ver4.4 is available as Ver4.4.1 Win / Mac.

PhysioDesigner 1.0 is available. PhysioDesigner can embed CellDesigner's SBML model into its multilevel physiological PrIML model. (2014/08/01)

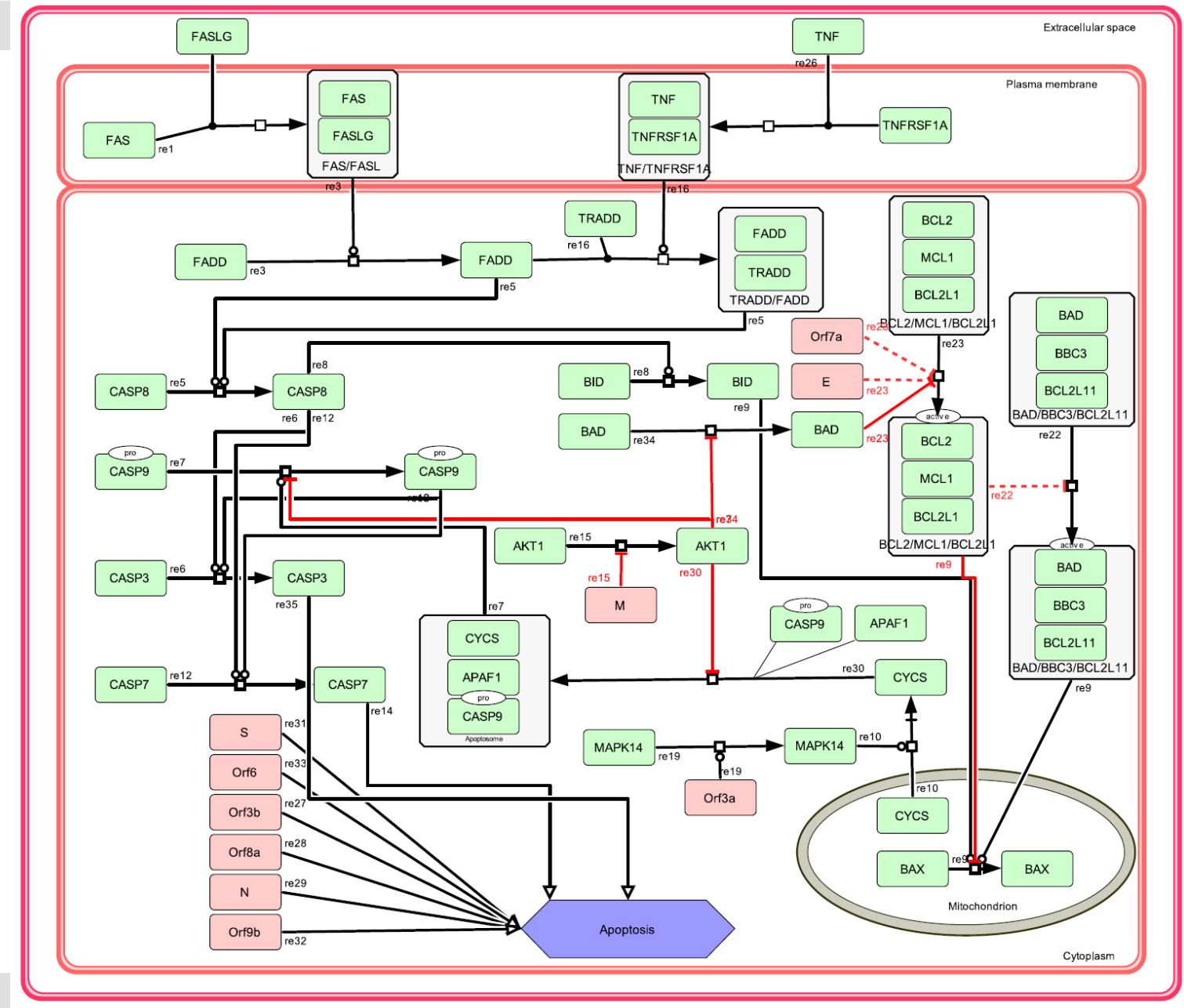
CellDesigner 4.4 is now available (2014/07/12)

Advertisement

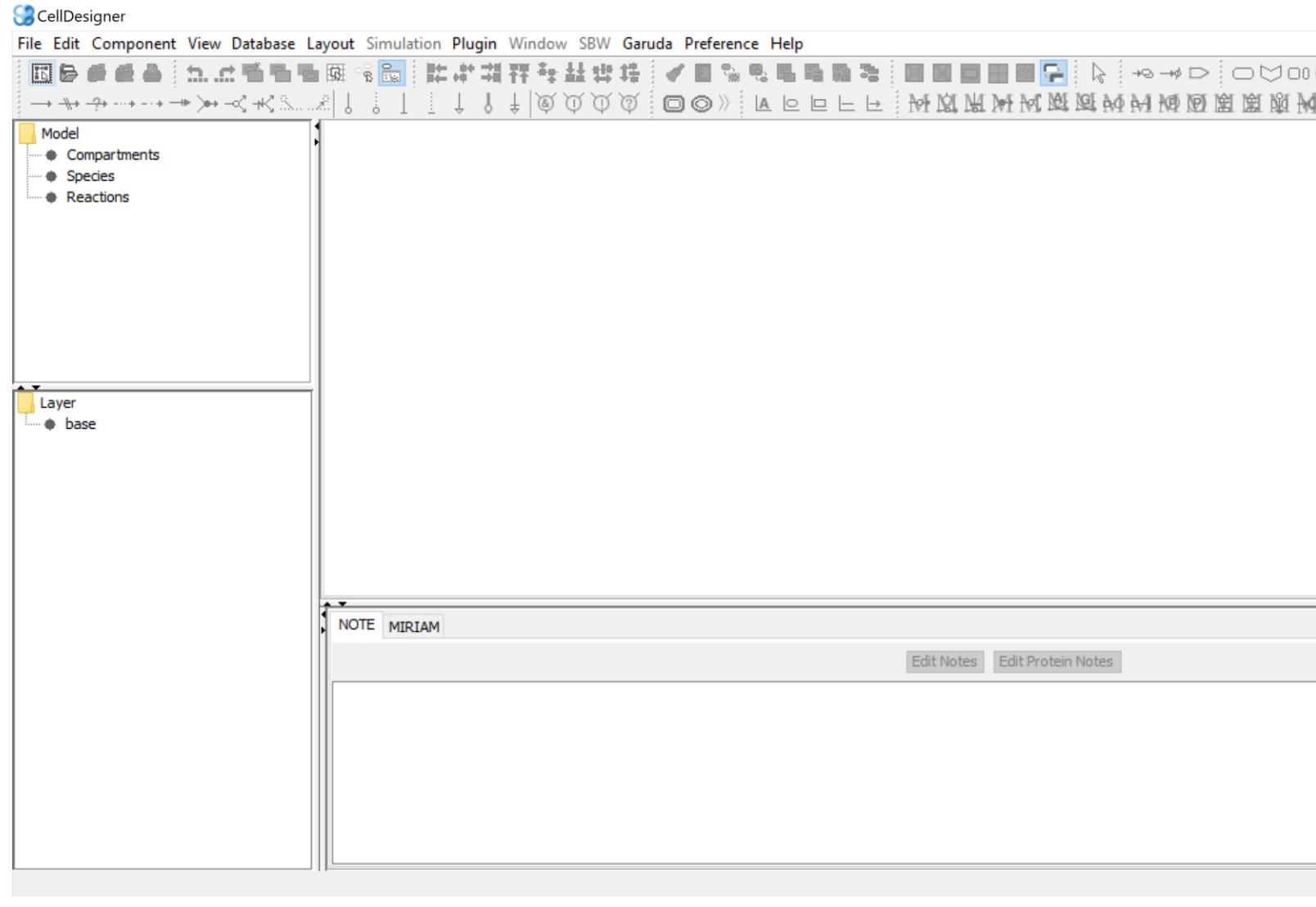
npj Systems Biology and Applications

Launching in 2015

EDITOR-IN-CHIEF
Hiroaki Kitano



Open the Apoptosis xml diagram in CellDesigner



Open in
CellDesigner

Select file

Regarder dans : Bureau

Accès rapide

- OneDrive
- Anna Niarakis
- Ce PC
- Bibliothèques
- Ce PC
- Réseau
- Acrobat Reader DC Raccourci

Nom de l'objet :

Types d'objets : All Files (*.*)

Select file

Regarder dans : Hands_On

Accès rapide

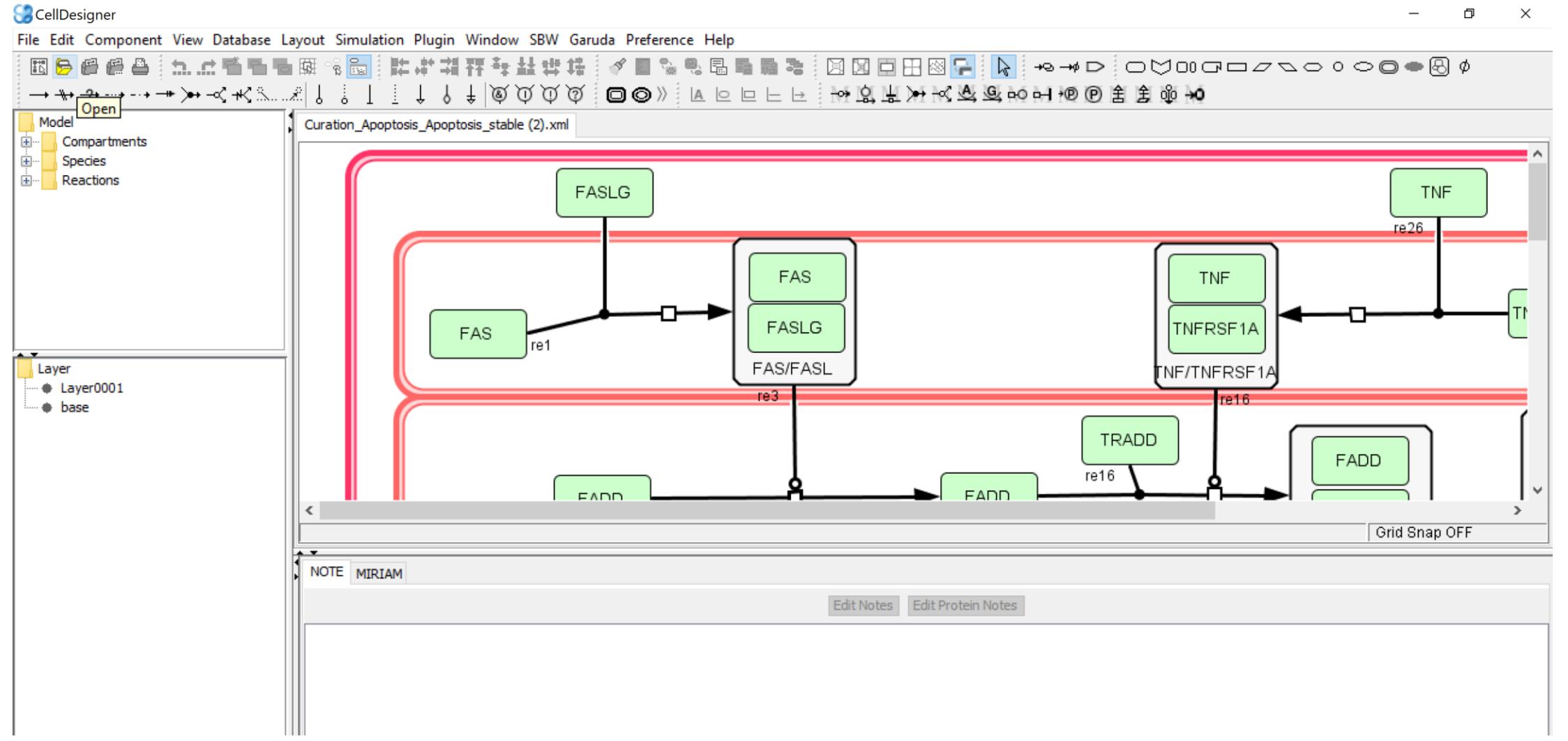
- Bureau
- Bibliothèques
- Ce PC
- Réseau

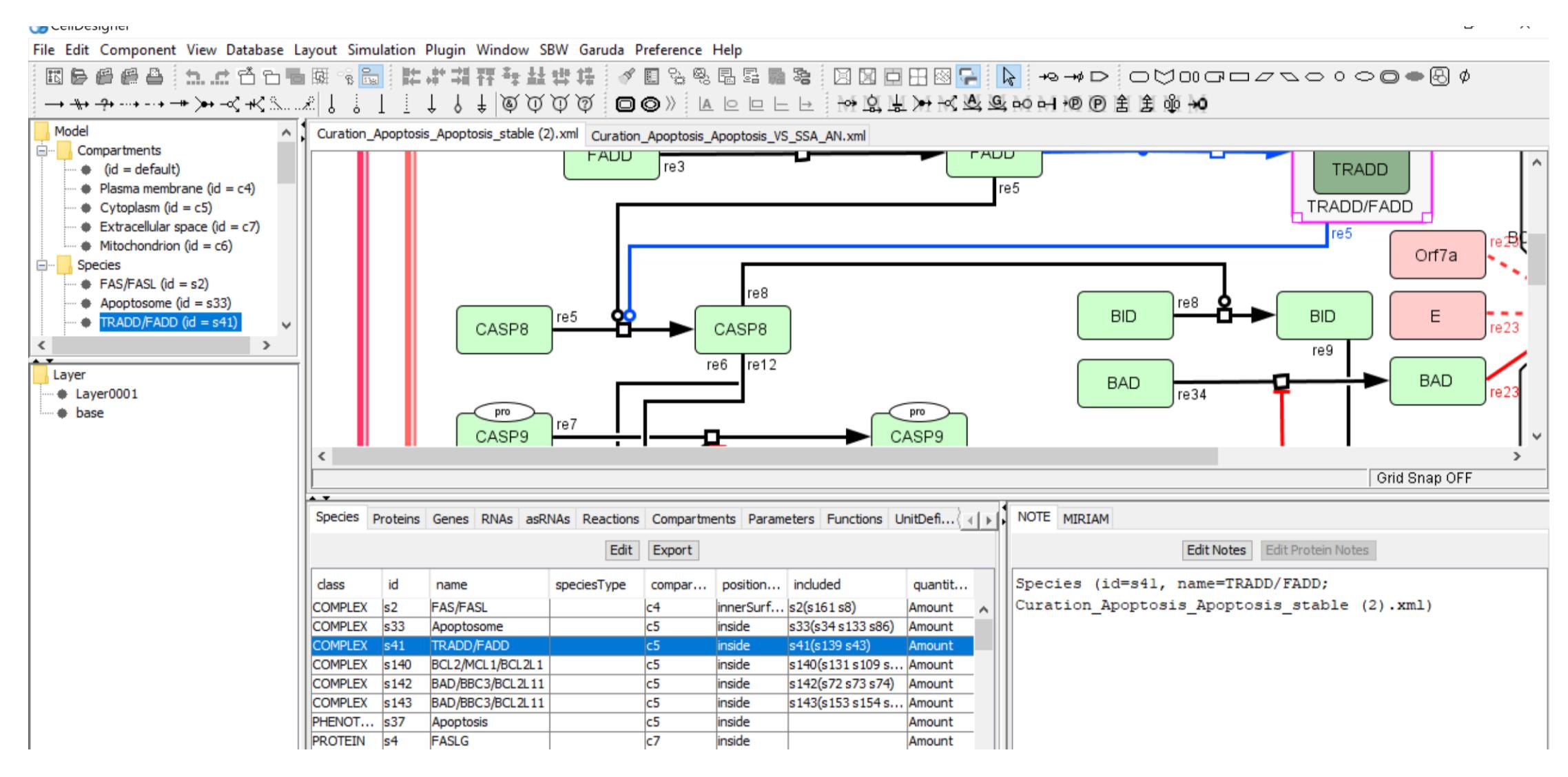
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Curation_Apoptosis_Apoptosis_stable (2)	01/11/2020 22:59	Document XML
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Executable Modules_SBML_qual_build_sif...	01/11/2020 23:03	BioLayout Express
tled (1)	01/11/2020 21:46	Chrome HTML Do...
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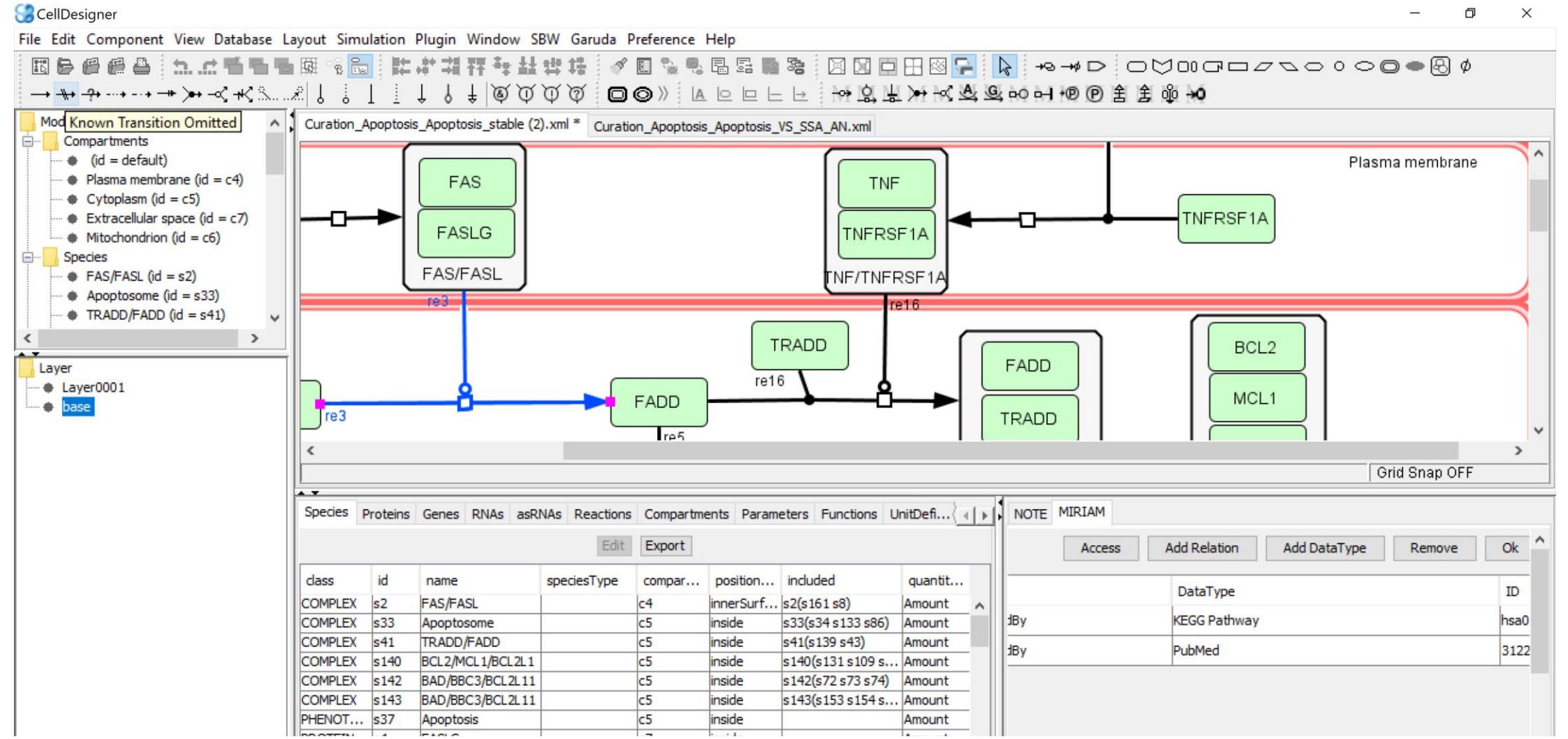
Nom de l'objet : Curation_Apoptosis_Apoptosis_stable (2)

Types d'objets : All Files (*.*)

Ouvrir Annuler







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1 <?xml version="1.0" encoding="UTF-8"?>
2 <sbml xmlns="http://www.sbml.org/sbml/level2/version4" xmlns:celldesigner="http://www.sbml.org/2001/ns/celldesigner" level="2" version="4">
3 <model metaid="Covid_19_apoptosis_21_04_2020" id="Covid_19_apoptosis_21_04_2020">
4 <notes>
5 <html xmlns="http://www.w3.org/1999/xhtml">
6 <head>
7 <title/>
8 </head>
9 <body>Vidisha Singh, GenHotel Laboratory, University of Evry-Paris Saclay, Evry, France
10 Apoptosis pathway for Covid-19 maps project is constructed by using the review paper of Fung&amp;Liu,2019,Annu rev micro (PMID=31226023).
11 KEGG pathway database is used to add reactions between the elements.
12 Map is constructed in the form of a cell including plasma membrane, cytoplasm in addition to extracellular space.
13 Ligands are present in the extracellular space which interacts with receptors in the plasma membrane to initiate signaling cascade in the cytoplasm.
14 All the map elements are named according to HGNC naming scheme.
15 All map reactions are annotated with PubMed Ids, KEGG pathway Ids using MIRIAM add relation&apos;bqbiol:isDescribedby&apos;.
16 MESH Id is provided for the phenotype &apos;Apoptosis&apos;.
17 </body>
18 </html>
19 </notes>
20 <annotation>
21 <celldesigner:extension>
22 <celldesigner:modelVersion>4.0</celldesigner:modelVersion>
23 <celldesigner:modelDisplay sizeX="1350" sizeY="1200"/>
24 <celldesigner:listOfIncludedSpecies>
25 <celldesigner:species id="s8" name="FASLG">
26 <celldesigner:notes>
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